

Gencore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.  
 protein - protein search, using sw model  
 on: September 20, 2004, 17:27:20 ; Search time 52 Seconds  
 (without alignments)  
 43.469 Million cell updates/sec  
 file: AUDET-SQ01  
 Effect score: 46  
 Sequence: 1 gsfifselw 8  
 Scoring table: BLOSUM62  
 Gapext 0.5  
 searched: 1586107 seqs, 282547505 residues  
 Ab1 / 0 / 5 Mat / hdm / a  
 Abb73180 Mat / hdm / a  
 Abb73183 Mat / hdm / a  
 Abb73171 Mat / hdm / a  
 Abb73182 Mat / hdm / a  
 Aay57799 TRAM-inte  
 Abb05528 Biotinyl  
 Aar54909 Immunodom  
 Aar54910 Immunodom  
 Aar89914 p53 prote  
 Aay06310 Human p53  
 AAY99001 HLA cIa  
 Ab22780 Human, any  
 Aab29161 Peptide #  
 Aab29159 Peptide #  
 Aab29167 Peptide #  
 Aab29160 Peptide #  
 Aab29117 Peptide #  
 Aag89730 p53 DR3, b  
 Aag89500 p53 DR 3.a  
 Aag89500 p53 DR 3.b

ALIGNMENTS

RESULT 1  
AAB86005

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SMARTES

S	Query	Match	Length	DB	ID	Description
sult No.	Score					
1	46	100.0	12	4	AAB86005	Aabb86005 DCM-assoc
2	46	100.0	13	4	AAB86006	Aabb86006 DCM-assoc
3	46	100.0	14	4	AAB86012	Aabb86012 DCM-assoc
4	46	100.0	14	4	AAB86013	Aabb86013 DCM-assoc
5	46	100.0	15	4	AAB86013	Aabb86013 DCM-assoc
6	46	100.0	15	4	AAB86021	Aabb86021 DCM-assoc
7	30	65.2	13	4	AAB86009	Aabb86009 DCM-assoc
8	30	65.2	13	4	AAB86007	Aabb86007 DCM-assoc
9	30	65.2	13	5	AA47221	AAm47221 Dilated C
10	30	65.2	15	4	AAB86028	Aabb86028 DCM auto
11	30	65.2	15	4	AAB86017	Aabb86017 DCM-assoc
12	30	65.2	15	4	AAB86014	Aabb86014 DCM-assoc
13	30	65.2	15	4	AAB86022	Aabb86022 DCM auto
14	30	65.2	15	5	AA020307	AA020307 Human pIe
15	29	63.0	15	6	ABJ37231	Abj37231 Rhodopsin
16	27	58.9	11	2	AAW11231	AAw11231 Peptide A
17	27	58.7	11	4	AAU27152	Aau27152 Human Leu
18	27	58.7	11	4	AAU26842	Aau26842 Human Leu
19	27	58.7	11	5	AAW52269	Aaw52269 Miniatute
20	27	58.7	12	2	AAW37188	Aaw37188 Human p53
21	27	58.7	12	2	AAW37188	Aaw37188 Human onc
22	27	58.7	12	2	AAW37189	Aaw37189 Ndm/hdm a
23	27	58.7	12	3	AAH17076	Aah17076 Ndm/hdm a
24	27	58.7	12	3	AAH17087	Aah17087 Ndm/hdm a
25	27	58.7	12	3	AAH17088	Aah17088 Ndm/hdm a
					Sequence 12 AA;	
					Query Match	100.0%
					Decc. Total similari-	100.0%
					ty	Decc. 0.0%

QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	KW XX Synthetic.
Db	1 GSFFSELW 8 2 GSFFSELW 9	AC XX Key Modified-site 14 FT /note= "Lys modified with an amide or free acid group"
RESULT 2		
AAB86006	AAB86006 standard; peptide; 13 AA.	FT XX PN WO200121660-A1.
ID		PD 29-MAR-2001.
XX		XX
AC		PF 21-SEP-2000; 2000WO-EP009241.
XX		XX
DT	12-JUL-2001 (first entry)	PR 21-SEP-1999; 99EP-00118630.
XX		PR 21-SEP-1999; 99EP-00118631.
DE	DCM-associated peptide #6.	PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX		XX
DCM; dilatative cardiomyopathy; autoantibody; cardiant;	Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;	PI
KW beta-1 adrenergic activated antibody; immunosuppressive.	OS Synthetic.	XX
XX		WPI; 2001-335469/35.
PN	WO200121660-A1.	DR XX
XX		PT New peptide useful for combating the autoantibodies that are responsible for dilatative cardiomyopathy.
PD	29-MAR-2001.	PT XX
XX		PS Claim 4; Page 22; 29pp; German.
PP	21-SEP-2000; 2000WO-EP009241.	XX
XX		This invention describes a novel peptide (P1) which can be used for (1) isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid phase; and (2) a chromatographic apparatus with (P1) bound. The products of the invention have cardiant and immunosuppressive activity. (P1) is used to produce medicine to combat beta-1 adrenergic activated autoantibodies having a causal pathological relationship with dilatative cardiomyopathy. This sequence represents a specifically claimed peptide used to illustrate the method of the invention
XX		SQ Sequence 14 AA;
PS	21-SEP-1999; 99EP-00118630.	Query Match Score 100.0%; Score 46; DB 4; Length 14; Best Local Similarity 100.0%; Pred. No. 0.075; Matches 0; Mismatches 0; Indels 0; Gaps 0;
PR	21-SEP-1999; 99EP-00118631.	XX
XX		QY 1 GSFFSELW 8 CC       Db 2 GSFFSELW 9
PA	(AFFI-) AFFINA IMMUNTECHNIK GMBH.	CC
XX		RESULT 4
PI	Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;	AA B86020
XX		ID AAB86020 standard; peptide; 14 AA.
DR	2001-335469/35.	XX
XX		AC AAB86020;
PS	New peptide useful for combating the autoantibodies that are responsible for dilatative cardiomyopathy.	XX
XX	Claim 3; Page 21; 29pp; German.	AC
PS		XX
XX	This invention describes a novel peptide (P1) which can be used for (1) isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid phase; and (2) a chromatographic apparatus with (P1) bound. The products of the invention have cardiant and immunosuppressive activity. (P1) is used to produce medicine to combat beta-1 adrenergic activated autoantibodies having a causal pathological relationship with dilatative cardiomyopathy. This sequence represents a specifically claimed peptide used to illustrate the method of the invention	DT 12-JUL-2001 (first entry)
XX		SQ Sequence 13 AA;
PS		Query Match Score 100.0%; Score 46; DB 4; Length 13; Best Local Similarity 100.0%; Pred. No. 0.069; Matches 0; Mismatches 0; Indels 0; Gaps 0;
XX		QY 1 GSFFSELW 8 CC       Db 3 GSFFSELW 10
XX		OS Synthetic.
XX		XX
XX		Key Modified-site 1 FT /note= "N-terminal acetylated"
AC	AAB86012;	FT 14 FT /note= "C-terminal amide"
XX		XX
DT	12-JUL-2001 (first entry)	DE PN DE19945211-A1.
XX		XX
DE	DCM-associated peptide #12.	PD 29-MAR-2001.
XX		XX
KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;		XX

PF 21-SEP-1999; 99DE-01045211.  
 XX PR 21-SEP-1999; 99DE-01045211.  
 XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 XX PA Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;  
 XX PI DR WPI; 2001-301259/32.  
 XX PT New autoantibody-binding peptides with an amino acid sequence  
 PT corresponding a beta-1-adrenergic receptor group useful for treating  
 PT dilatative cardiomyopathy.  
 XX SQ PS Claim 2; Page 5; 8pp; German.

XX This invention describes novel peptides (I) with an amino acid sequence corresponding a beta-1-adrenergic receptor group recognized by autoantibodies associated with dilatative cardiomyopathy (DCM). The invention also describes a chromatographic device comprising (I) bound to a solid phase. The products of the invention have cardiotropic activity. (I) are useful for treating DCM by binding autoantibodies directed against myocardial beta-1-adrenergic receptor, either by neutralizing the antibodies *in vivo* or by extracorporeal treatment of blood or plasma with (I) immobilized on a solid phase. This sequence represents a specifically claimed peptide used to illustrate the method of the invention

XX SQ Sequence 14 AA;

Query Match Score 46; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.075;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSFFSELW 8  
 Db 2 GSFFSELW 9

RESULT 5  
 ID AAB86013 standard; peptide; 15 AA.  
 XX AC AAB86013;  
 XX DT 12-JUL-2001 (first entry)  
 DE DCM-associated peptide #13.  
 KW DCM; dilatative cardiomyopathy; autoantibody; cardiotropic;  
 KW beta-1 adrenergic activated antibody; immunosuppressive.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetylated"  
 FT Modified-site 15 /note= "C-terminal amide".  
 XX DT 12-JUL-2001 (first entry)  
 DE DCM-associated peptide #13.  
 KW DCM; dilatative cardiomyopathy; autoantibody; cardiotropic;  
 KW beta-1 adrenergic activated antibody; immunosuppressive.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 15 /note= "Lys modified with an amide or free acid group"  
 XX PR 21-SEP-1999; 99EP-00118630.  
 XX PR 21-SEP-1999; 99EP-00118631.  
 XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 XX PA Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;  
 XX PI DR WPI; 2001-335469/35.  
 XX PT New peptide useful for combating the autoantibodies that are responsible

PT for dilatative cardiomyopathy.  
 XX PS Claim 4; Page 22; 29pp; German.

XX This invention describes a novel peptide (P1) which can be used for (1) isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid phase; and (2) a chromatographic apparatus with (P1) bound. The products of the invention have cardiotropic and immunosuppressive activity. (P1) is used to produce medicine to combat beta-1 adrenergic activated autoantibodies having a causal pathological relationship with dilatative cardiomyopathy. This sequence represents a specifically claimed Peptide used to illustrate the method of the invention

XX SQ Sequence 15 AA;

Query Match Score 46; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.08;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSFFSELW 8  
 Db 3 GSFFSELW 10

RESULT 6  
 ID AAB86021 standard; peptide; 15 AA.  
 XX AC AAB86021;  
 XX DT 12-JUL-2001 (first entry)  
 DE DCM autoantibody-associated peptide #2.  
 KW DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiotropic;  
 KW autoantibody; myocardial.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetylated"  
 FT Modified-site 15 /note= "C-terminal amide".  
 XX DT 12-JUL-2001 (first entry)  
 DE DCM autoantibody-associated peptide #2.  
 KW DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiotropic;  
 KW autoantibody; myocardial.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "Lys modified with an amide or free acid group"  
 XX PR 21-SEP-1999; 99DE-01045211.  
 XX PR 21-SEP-1999; 99EP-00118630.  
 XX PR 21-SEP-1999; 99EP-00118631.  
 XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 XX PA Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;  
 XX PI DR WPI; 2001-301259/32.  
 XX PT New autoantibody-binding peptides with an amino acid sequence  
 PT corresponding a beta-1 adrenergic receptor group useful for treating  
 PT dilatative cardiomyopathy.

XX PS Claim 2; Page 5; 8pp; German.

XX This invention describes novel peptides (I) with an amino acid sequence corresponding a beta-1 adrenergic receptor group recognized by autoantibodies associated with dilatative cardiomyopathy (DCM). The invention also describes a chromatographic device comprising (I) bound to a solid phase. The products of the invention have cardiotropic activity. (I) are useful for treating DCM by binding autoantibodies directed against myocardial beta-1 adrenergic receptors, either by neutralizing the antibodies *in vivo* or by extracorporeal treatment of blood or plasma with

CC (1) immobilized on a solid phase. This sequence represents a specifically  
CC claimed peptide used to illustrate the method of the invention  
XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 46; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.08;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OS Synthetic.  
SYN 1 GSFFSEBLW 8  
| : | : | : |  
DB 3 GSFFSEBLW 10

RESULT 7

AAB86009 standard; peptide; 13 AA.

ID AAB86009

AC AAB86009;

XX

DT 12-JUL-2001 (first entry)

DE DCM-associated peptide #7.

XX

KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;

beta-1 adrenergic activated antibody; immunosuppressive.

XX

OS Synthetic.

XX

PN WO200121660-A1.

XX

PD 29-MAR-2001.

XX

PP 21-SEP-2000; 2000WO-EP009241.

XX

PR 21-SEP-1999; 99EP-00118630.

XX

PR 21-SEP-1999; 99EP-00118631.

XX

PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.

XX

PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;

XX

DR WPI; 2001-335469/35.

XX

PT New peptide useful for combating the autoantibodies that are responsible

for dilatative cardiomyopathy.

XX

PS Claim 3; Page 21; 29pp; German.

XX

QQ Sequence 13 AA;

XX

DR Query Match 65.2%; Score 30; DB 4; Length 13;

XX

PR Best Local Similarity 50.0%; Pred. No. 70;

XX

PT Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

XX

PS QY 1 GSFFSEBLW 8

| : | : |

DB 3 GTLFSSDFW 10

XX

PD 12-FEB-2002 (first entry)

XX

DE dilated cardiomyopathy absorbents related peptide #1.

XX

KW Dilated cardiomyopathy; absorbent; betal adrenoreceptor;

XX

M2 muscarine receptor; antibody.

XX

OS Synthetic.

XX

PN WO200176662-A1.

XX

PD 18-OCT-2001.

XX

PR 09-APR-2001; 2001WO-JP003026.

XX

PT 07-APR-2000; 2000JP-00106915.

XX

PR 07-APR-2000; 2000JP-00106915.

XX

PR 07-APR-2000; 2000JP-00106915.

XX

PR 07-APR-2000; 2000JP-00106915.

XX

CC (1) immobilized on a solid phase. This sequence represents a specifically  
CC claimed peptide used to illustrate the method of the invention

XX

SQ Sequence 15 AA;

XX

Query Match 65.2%; Score 30; DB 4; Length 13;

XX

Best Local Similarity 50.0%; Pred. No. 70;

XX

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

XX

OS Synthetic.

XX

PN WO200176662-A1.

XX

PD 18-OCT-2001.

XX

PR 09-APR-2001; 2001WO-JP003026.

XX

PT 07-APR-2000; 2000JP-00106915.

XX

PR 07-APR-2000; 2000JP-00106915.

XX

CC (1) immobilized on a solid phase. This sequence represents a specifically  
CC claimed peptide used to illustrate the method of the invention

XX

SQ Sequence 15 AA;

XX

Query Match 65.2%; Score 30; DB 4; Length 13;

XX

Best Local Similarity 50.0%; Pred. No. 70;

XX

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

XX

OS Synthetic.

XX

PN WO200176662-A1.

XX

PD 18-OCT-2001.

XX

PR 09-APR-2001; 2001WO-JP003026.

XX

PT 07-APR-2000; 2000JP-00106915.

XX

PR 07-APR-2000; 2000JP-00106915.

XX

XX (KANF ) KANEKA CORP.  
 XX Ogino E, Furuyoshi S, Hirai F, Nishimoto T;  
 XX WPI; 2002-041274/05.

PT Adsorbents for dilated cardiomyopathy, comprises an immobilized compound  
 PT capable of selectively removing antibodies against approximately bi  
 PT adrenoceptor and/or M2 muscarine receptors in body fluid without  
 PT pretreatment.

XX PS Claim 3; Page 21; 37pp; Japanese.

XX The present invention relates to a method of immobilising an adsorbent  
 CC with a compound capable of binding to an antibody against betal  
 CC adrenoceptor and/or an antibody against M2 muscarine receptor on a  
 CC water-insoluble support. The adsorbents, apparatus and method are useful  
 CC for treating dilated cardiomyopathy by removing antibodies against betal  
 CC adrenoceptor and/or M2 muscarine receptor. The present sequence is a  
 CC peptide described in the exemplification of the invention

XX Sequence 13 AA;

Query Match 65.2%; Score 30; DB 5; Length 13;  
 Best Local Similarity 85.7%; Pred. No. 70;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSFFSEL 7  
 Db 7 GSFFECEL 13

RESULT 10  
 AAB86028  
 ID AAB86028 standard; peptide; 15 AA.  
 AC AAB86028;  
 XX DT 12-JUL-2001 (first entry)  
 XX DE DCM autoantibody-associated peptide #2.  
 KW DCM; autoantibody; betal-adrenergic receptor; dilatative cardiomyopathy;  
 KW cardiant; myocardial.  
 XX OS Synthetic.

Key Modified-site 1  
 FT /note= "N-terminal acetylated"  
 FT Modified-site 15  
 FT /note= "C-terminal amide"  
 XX DN DE19945210-A1.  
 XX PD 29-MAR-2001.  
 XX PF 21-SEP-1999; 99DE-01045210.  
 XX PR 21-SEP-1999; 99DE-01045210.

PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;  
 XX WPI; 2001-301258/32.

XX New autoantibody-binding peptides with an amino acid sequence  
 PT corresponding a betal-adrenergic receptor group, useful for treating  
 PT dilatative cardiomyopathy.

XX PS Claim 2; Page 5; 8pp; German.

XX Query Match 65.2%; Score 30; DB 4; Length 15;

XX This invention describes novel peptides (I) with an amino acid sequence  
 CC corresponding a betal-1 adrenergic receptor group recognized by  
 CC autoantibodies associated with dilatative cardiomyopathy (DCM). The  
 CC products of the invention have cardiant activity. (I) are useful for  
 CC treating DCM by binding autoantibodies directed against myocardial betal-1  
 CC -adrenergic receptors, either by neutralizing the antibodies in vivo or  
 CC by extracorporeal treatment of blood or plasma with (I) immobilized on a  
 CC solid phase. This sequence represents a specifically claimed peptide used  
 CC to illustrate the method of the invention  
 XX Sequence 15 AA;

Query Match 65.2%; Score 30; DB 4; Length 15;

Best Local Similarity 50.0%; Pred. No. 81;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSFFSELW 8  
 2 : | : |  
 3 GTLFSDFW 10

RESULT 11  
 AAB86017  
 ID AAB86017 standard; peptide; 15 AA.  
 AC AAB86017;  
 XX DT 12-JUL-2001 (first entry)  
 DE DCM-associated peptide #17.

KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;  
 KW betal-1 adrenergic activated antibody; immunosuppressive.

XX OS Synthetic.

Key FH  
 FT Modified-site 15  
 FT /note= "Lys modified with an amide or free acid group"

XX PN WO200121660-A1.  
 XX PD 29-MAR-2001.  
 XX PF 21-SEP-2000; 2000WO-EP009241.  
 XX PR 21-SEP-1999; 99EP-00118630.  
 XX PR 21-SEP-1999; 99EP-00118631.

PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;  
 XX WPI; 2001-335469/35.

XX DR  
 PT New peptide useful for combating the autoantibodies that are responsible  
 PT for dilatative cardiomyopathy.

XX PS Claim 4; Page 22; 29pp; German.

XX This invention describes a novel peptide (P1) which can be used for (1)  
 CC isolating betal-1 adrenergic activated antibodies bound to (P1) on a solid  
 CC phase; and (2) a chromatographic apparatus with (P1) bound to (P1) is  
 CC of the invention have cardiant and immunosuppressive activity. (P1) is  
 CC used to produce medicine to combat beta 1 adrenergic activated  
 CC autoantibodies having a causal pathological relationship with dilatative  
 CC cardiomyopathy. This sequence represents a specifically claimed peptide  
 CC used to illustrate the method of the invention  
 XX Sequence 15 AA;

Query Match 65.2%; Score 30; DB 4; Length 15;



PD 12-DEC-2001.  
 XX PS Example 5; Page 18 (Disclosure); 31pp; Chinese.  
 CC The invention relates to the novel polypeptide-human plectin 10, the  
 CC polynucleotide encoding it, the process for preparing the polypeptide by  
 CC DNA recombination, the application of the polypeptide in treating  
 CC diseases such as cancer and HIV infection. The invention also relates to  
 CC the antagonist of the polypeptide and its medical action, and the  
 CC application of the polynucleotide. This sequence represents an N-terminal  
 CC region of the human plectin 10 protein of the invention  
 XX SQ Sequence 15 AA:  
 PT Polypeptide-human plectin 10 and polynucleotide encoding it.  
 XX PS Example 5; Page 18 (Disclosure); 31pp; Chinese.  
 CC The invention relates to the novel polypeptide-human plectin 10, the  
 CC polynucleotide encoding it, the process for preparing the polypeptide by  
 CC DNA recombination, the application of the polypeptide in treating  
 CC diseases such as cancer and HIV infection. The invention also relates to  
 CC the antagonist of the polypeptide and its medical action, and the  
 CC application of the polynucleotide. This sequence represents an N-terminal  
 CC region of the human plectin 10 protein of the invention  
 XX SQ Sequence 15 AA:  
 Query Match 65.2%; Score 30; DB 5; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 81;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 SFFSELW 8  
 Db 2 AFFSSIW 8

---

RESULT 15  
 ABJ3731  
 ID ABJ3731 standard; peptide; 15 AA.  
 XX AC ABJ3731;  
 XX DT 08-MAY-2003 (First entry)  
 XX DE Rhodopsin related G-protein coupled receptor binding site peptide #107.  
 XX KW Compound library; microenvironment; G-protein Coupled Receptor; GPCR;  
 KW Rhodopsin.  
 XX Unidentified.  
 XX PN W02003004147-A2.  
 XX PD 16-JAN-2003.  
 XX PR 05-JUL-2002; 2002WO-GB003094.  
 XX PR 06-JUL-2001; 2001GB-00016570.  
 XX PA (BIOF-) BIOFOCUS PLC.  
 PI Crossley R, Rose VS, Stevens AP;  
 XX DR WPI; 2003-221549/21.  
 XX PS Producing compound library, by generating biological target model using  
 PT target sequence information, defining microenvironments interacting with  
 PT ligand and motifs interacting with microenvironment, and assembling  
 PT motifs.  
 XX Disclosure; Fig 1; 39pp; English.  
 XX The invention relates to a novel method for producing a compound library.  
 CC The novel method involves reducing a biological target into a group of

Blank

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2004, 17:31:56 ; Search time 124 Seconds  
(without alignments) ; 20.718 Million cell updates/sec

Title: AUDET-SEQ1  
Perfect score: 46  
Sequence: 1 gsfffselw 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1342398 seqs, 322133274 residues

Total number of hits satisfying chosen parameters: 58621

Minimum DB seq length: 11  
Maximum DB seq length: 15

Post-processing: Minimum March 0%  
Maximum March 100%  
Listing first 45 summaries

Database : Published Applications\_AA:  
 1: /cn2\_6/ptodata/1/pubbaa/us07\_PUBCOMB.pep:  
 2: /cn2\_6/ptodata/1/pubbaa/PCT\_NEW\_PUB.pep:  
 3: /cn2\_6/ptodata/1/pubbaa/us06\_PUB.pep:  
 4: /cn2\_6/ptodata/1/pubbaa/us05\_PUBCOMB.pep:  
 5: /cn2\_6/ptodata/1/pubbaa/us07\_NEW\_PUB.pep:  
 6: /cn2\_6/ptodata/1/pubbaa/PCTUS\_PUBCOMB.pep:  
 7: /cn2\_6/ptodata/1/pubbaa/us08\_NEW\_PUB.pep:  
 8: /cn2\_6/ptodata/1/pubbaa/us09\_PUBCOMB.pep:  
 9: /cn2\_6/ptodata/1/pubbaa/us09B\_PUBCOMB.pep:  
 10: /cn2\_6/ptodata/1/pubbaa/us09B\_PUBCOMB.pep:  
 11: /cn2\_6/ptodata/1/pubbaa/us09C\_PUBCOMB.pep:  
 12: /cn2\_6/ptodata/1/pubbaa/us10A\_NEW\_PUB.pep:  
 13: /cn2\_6/ptodata/1/pubbaa/us10A\_PUBCOMB.pep:  
 14: /cn2\_6/ptodata/1/pubbaa/us10B\_PUBCOMB.pep:  
 15: /cn2\_6/ptodata/1/pubbaa/us10C\_PUBCOMB.pep:  
 16: /cn2\_6/ptodata/1/pubbaa/us10\_NEW\_PUB.pep:  
 17: /cn2\_6/ptodata/1/pubbaa/us60\_NEW\_PUB.pep:  
 18: /cn2\_6/ptodata/1/pubbaa/us60\_PUBCOMB.pep:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match	Length	DB ID	Description
1	30	65.2	13	16	US-10-221-042-1	Sequence 1, Appli
2	28	60.9	14	14	US-09-964-821B-53	Sequence 53, Appli
3	28	60.9	14	14	US-10-268-332-53	Sequence 53, Appli
4	27	58.7	11	10	US-09-840-085-31	Sequence 31, Appli
5	27	58.7	12	9	US-09-214-371-17	Sequence 17, Appli
6	27	58.7	12	9	US-09-214-371-24	Sequence 24, Appli
7	27	58.7	12	9	US-09-214-371-25	Sequence 25, Appli
8	27	58.7	12	12	US-10-609-217-131	Sequence 121, Appli
9	27	58.7	12	12	US-10-609-217-132	Sequence 122, Appli
10	27	58.7	12	12	US-10-609-217-143	Sequence 143, Appli
11	27	59.7	12	12	US-10-609-217-144	Sequence 144, Appli
12	27	58.7	12	12	US-10-632-388-131	Sequence 131, Appli
13	27	58.7	12	12	US-10-632-388-132	Sequence 132, Appli
14	27	58.7	12	12	US-10-632-388-143	Sequence 143, Appli
15	27	58.7	12	12	US-10-632-388-144	Sequence 144, Appli

**ALIGNMENTS**

RESULT 1  
US-10-221-042-1  
; Sequence 1, Application US/10221042  
; General Information:  
; Publication No. US20040120946A1  
; Applicant: KANKEA CORPORATION  
; Title of Invention: ADSORBENTS FOR DILATED CARDIOMYOPATHY  
; File Reference: 12218/5  
; Current Application Number: US/10/221,042  
; Current Filing Date: 2002-10-09  
; Prior Application Number: PCT/JP01/03026  
; Prior Filing Date: 2001-04-09  
; Prior Application Number: JP 2000-106915  
; Prior Filing Date: 2000-04-07  
; Software: PatentIn Version 3.1  
; Number of SEQ ID Nos: 13  
; SEQ ID NO 1  
; Length: 13  
; Type: PRT  
; Organism: Artificial  
; Other Information: peptide  
; Feature:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match	Length	DB ID	Description
1	30	65.2	13	16	US-10-221-042-1	Sequence 1, Appli
2	28	60.9	14	14	US-09-964-821B-53	Sequence 53, Appli
3	28	60.9	14	14	US-10-268-332-53	Sequence 53, Appli
4	27	58.7	11	10	US-09-840-085-31	Sequence 31, Appli
5	27	58.7	12	9	US-09-214-371-17	Sequence 17, Appli
6	27	58.7	12	9	US-09-214-371-24	Sequence 24, Appli
7	27	58.7	12	9	US-09-214-371-25	Sequence 25, Appli
8	27	58.7	12	12	US-10-609-217-131	Sequence 121, Appli
9	27	58.7	12	12	US-10-609-217-132	Sequence 122, Appli
10	27	58.7	12	12	US-10-609-217-143	Sequence 143, Appli
11	27	59.7	12	12	US-10-609-217-144	Sequence 144, Appli
12	27	58.7	12	12	US-10-632-388-131	Sequence 131, Appli
13	27	58.7	12	12	US-10-632-388-132	Sequence 132, Appli
14	27	58.7	12	12	US-10-632-388-143	Sequence 143, Appli
15	27	58.7	12	12	US-10-632-388-144	Sequence 144, Appli

Query Match Best Local Similarity Score 30; DB 16; Length 13;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSFFSEEL 7  
Db 7 GSFFCEEL 13

RESULT 2  
US-09-964-821B-53  
Sequence 53, Application US/099649821B  
Publication No. US20030186360A1  
GENERAL INFORMATION:  
APPLICANT: FEDER, J. N.  
APPLICANT: MINTIER, G.  
APPLICANT: RAMANATHAN, C. S.  
APPLICANT: HAWKEN, D. R.  
APPLICANT: CACACE, A.  
APPLICANT: BARBER, L.  
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3,  
FILE REFERENCE: D0042NP  
CURRENT APPLICATION NUMBER: US/09/964, 821B  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: 60/235, 713  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/261, 783  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/305, 085  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: 60/313, 171  
PRIOR FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 53  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: polypeptide  
US-09-964-821B-53

Query Match Score 28; DB 10; Length 14;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFSEELW 8  
Db 6 SFSEELW 12

RESULT 3  
US-10-268-332-53  
Sequence 53, Application US/10268332  
Publication No. US20030175748A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3, EXPRESSED HIGHLY  
FILE REFERENCE: D0042A CIP  
CURRENT APPLICATION NUMBER: US/10/268, 332  
PRIOR APPLICATION NUMBER: U.S. 60/235, 713  
PRIOR FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: U.S. 60/261, 783  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: U.S. 60/305, 085  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: U.S. 60/313, 171  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: U.S. 09/964, 821  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 53  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-268-332-53

Query Match Score 28; DB 14; Length 14;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFSEELW 8  
Db 6 SFSEELW 12

RESULT 4  
US-09-840-085-31  
Sequence 31, Application US/09840085  
GENERAL INFORMATION:  
APPLICANT: Schebartz Shrader, Alanna  
APPLICANT: Chin, Jason W. K.  
APPLICANT: Zutshi Reena  
APPLICANT: Cutledge, Stacey E.  
APPLICANT: Kenibbeck Martin, Joanne D.  
APPLICANT: Zondlo, Neal J.  
TITLE OF INVENTION: DNA and Protein Binding Miniature Proteins  
CURRENT APPLICATION NUMBER: US/09/840, 085  
CURRENT FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: US 60/199, 408  
PRIOR FILING DATE: 2000-04-24  
FILE REFERENCE: 44574-5099-US  
CURRENT APPLICATION NUMBER: US/09/840, 085  
CURRENT FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: US 60/240, 566  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US PROVISIONAL  
PRIOR FILING DATE: 2001-01-13  
PRIOR APPLICATION NUMBER: US PROVISIONAL  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: Patentin ver. 2.1  
SEQ ID NO 31  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: p53 miniature  
OTHER INFORMATION: protein p53AD  
US-09-840-085-31

Query Match Score 27; DB 10; Length 11;  
Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSEELW 8  
Db 3 SFSEELW 7

RESULT 5  
US-06-214-371-17  
Sequence 17, Application US/09214371B  
Patent No. US20010018511A1  
GENERAL INFORMATION:  
APPLICANT: Lane, David  
APPLICANT: Bottger, Volker  
APPLICANT: Bottger, Angelica  
APPLICANT: Picklesley, Stephen  
APPLICANT: Chene, Patrick  
APPLICANT: Hochkeppel, Heinz-Kurt  
APPLICANT: Garcia-Echeverria, Carlos  
APPLICANT: Furset, Pascal  
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2  
FILE REFERENCE: 4-20937/A/PCT  
CURRENT APPLICATION NUMBER: US/09/214, 371B  
CURRENT FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: PCT/EP97/03549  
PRIOR FILING DATE: 1997-07-04  
NUMBER OF SEQ ID NOS: 83

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-17

Qy   4 FSELW 8
Db   4 FSIDLW 8

RESULT 6
US-09-214-371-24
Sequence 24, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Heinz-Kurt
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Angelica
; APPLICANT: Garcia-Echeverria, Carlos
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Ac-Gln
; SEQ ID NO 25
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: Ac-Gln
; NAME/KEY: VARIANT
; LOCATION: (12)
; OTHER INFORMATION: X = Pro-NH2
US-09-214-371-25

Query Match      58.7%; Score 27; DB 9; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   4 FSELW 8
Db   4 FSIDLW 8

RESULT 8
US-10-609-217-131
Sequence 131, Application US/10609217
Publication No. US20040044188A1
GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-227
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SEQ ID NO 131
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-131

Query Match      58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   4 FSELW 8
Db   4 FSIDLW 8

RESULT 7
US-09-214-371-25
Sequence 25, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Chene, Stephen
; APPLICANT: Hochkeppel, Angelica
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Heinz-Kurt
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Angelica
; APPLICANT: Garcia-Echeverria, Carlos
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: Ac-Gln
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Ac-Gln
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: VARIANT
; LOCATION: (12)
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: Pro-NH2
US-09-214-371-24

Query Match      58.7%; Score 27; DB 9; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   4 FSELW 8
Db   4 FSIDLW 8

RESULT 9
US-10-609-217-132
Sequence 132, Application US/10609217
Publication No. US20040044188A1
GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Chene, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt

```

GENERAL INFORMATION:  
*i* APPLICANT: FEIGE, ULRICH  
*i* APPLICANT: LIU, CHUAN-FA  
*i* APPLICANT: CHEETHAM, JANET C.  
*i* APPLICANT: BOONE, THOMAS CHARLES  
*i* TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
*i* FILE REFERENCE: A-527  
*i* CURRENT APPLICATION NUMBER: US/10/609,217  
*i* CURRENT FILING DATE: 2003-06-27  
*i* PRIORITY NUMBER: US/09/428,082B  
*i* PRIOR FILING DATE: 1999-10-22  
*i* PRIOR APPLICATION NUMBER: 60/105,371  
*i* PRIOR FILING DATE: 1998-10-23  
*i* NUMBER OF SEQ ID NOS: 1133  
*i* SOFTWARE: PatentIn version 3.1  
*i* SEQ ID NO: 132  
*i* LENGTH: 12  
*i* TYPE: PRT  
*i* ORGANISM: Artificial Sequence  
*i* FEATURE:  
*i* OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE  
US-10-609-217-132

Query Match 58.7%; Score 27; DB 12; Length 12;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0;  
Gaps 0;

QY 4 FSBLW 8  
Db 4 FSDLW 8

RESULT 10  
US-10-609-217-143

Sequence 143, Application US/10609217  
*i* Publication No. US20040044188A1  
GENERAL INFORMATION:  
*i* APPLICANT: FEIGE, ULRICH  
*i* APPLICANT: LIU, CHUAN-FA  
*i* APPLICANT: CHEETHAM, JANET C.  
*i* APPLICANT: BOONE, THOMAS CHARLES  
*i* TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
*i* FILE REFERENCE: A-527  
*i* CURRENT APPLICATION NUMBER: US/10/609,217  
*i* CURRENT FILING DATE: 2003-06-27  
*i* PRIORITY NUMBER: US/09/428,082B  
*i* PRIOR FILING DATE: 1999-10-22  
*i* PRIOR APPLICATION NUMBER: 60/105,371  
*i* PRIOR FILING DATE: 1998-10-23  
*i* NUMBER OF SEQ ID NOS: 1133  
*i* SOFTWARE: PatentIn version 3.1  
*i* SEQ ID NO: 143  
*i* LENGTH: 12  
*i* TYPE: PRT  
*i* ORGANISM: Artificial Sequence  
*i* FEATURE:  
*i* OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE  
US-10-609-217-143

Query Match 58.7%; Score 27; DB 12; Length 12;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0;  
Gaps 0;

QY 4 FSBLW 8  
Db 4 FSDLW 8

RESULT 11  
US-10-609-217-144

Sequence 144, Application US/10609217  
*i* Publication No. US20040044188A1  
GENERAL INFORMATION:  
*i* APPLICANT: FEIGE, ULRICH

RESULT 13  
US-10-632-388-132

Sequence 132, Application US/10632338  
*i* Publication No. US20040053845A1  
GENERAL INFORMATION:  
*i* APPLICANT: FEIGE, ULRICH  
*i* APPLICANT: LIU, CHUAN-FA  
*i* APPLICANT: CHEETHAM, JANET C.  
*i* APPLICANT: BOONE, THOMAS CHARLES  
*i* TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
*i* FILE REFERENCE: A-527  
*i* CURRENT APPLICATION NUMBER: US/10/632,388  
*i* CURRENT FILING DATE: 2003-07-31  
*i* PRIORITY NUMBER: US/09/428,082B  
*i* PRIOR FILING DATE: 1999-10-22  
*i* PRIOR APPLICATION NUMBER: 60/105,371  
*i* PRIOR FILING DATE: 1998-10-23  
*i* NUMBER OF SEQ ID NOS: 1133  
*i* SOFTWARE: PatentIn version 3.1  
*i* SEQ ID NO: 131  
*i* LENGTH: 12  
*i* TYPE: PRT  
*i* ORGANISM: Artificial Sequence  
*i* FEATURE:  
*i* OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE  
US-10-632-388-131

Query Match 58.7%; Score 27; DB 12; Length 12;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0;  
Gaps 0;

QY 4 FSBLW 8  
Db 4 FSDLW 8

```

; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-132

Query Match Similarity 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4 FSEIW 8
          ||:|
Db 4 FSDIW 8

RESULT 14
US-10-632-388-143
; Sequence 143, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-143

Query Match Similarity 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4 FSEIW 8
          ||:|
Db 4 FSDIW 8

RESULT 15
US-10-632-388-144
; Sequence 144, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA

```

B  
lank

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2004, 17:30:00 ; Search time 17 Seconds  
(without alignments)  
24.295 Million cell updates/sec

Title: AUDET-SEQ1  
Perfect score: 46  
Sequence: 1 gffffselw 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 42678

Minimum DB seq length: 11  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgmn2\_6/pctodata/2/iaa/5A\_COMB.pep:\*

2: /cgmn2\_6/pctodata/2/iaa/5B\_COMB.pep:\*

3: /cgmn2\_6/pctodata/2/iaa/6A\_COMB.pep:\*

4: /cgmn2\_6/pctodata/2/iaa/6B\_COMB.pep:\*

5: /cgmn2\_6/pctodata/2/iaa/PCTNS\_COMB.pep:\*

6: /cgmn2\_6/pctodata/2/iaa/backtless1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

%

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	30	65.2	11	1 US-08-424-957-42	Sequence 42, App1
2	30	65.2	11	3 US-09-035-686-43	Sequence 42, App1
3	27	58.7	11	1 US-09-428-082B-131	Sequence 131, App1
4	27	58.7	11	1 US-09-428-082B-132	Sequence 132, App1
5	27	58.7	11	4 US-09-428-082B-143	Sequence 143, App1
6	27	58.7	11	4 US-09-428-082B-144	Sequence 144, App1
7	27	58.7	11	1 US-08-277-660A-1	Sequence 1, App1
8	27	58.7	11	1 US-08-277-660A-4	Sequence 4, App1
9	27	58.7	11	1 US-08-277-660A-4	Sequence 4, App1
10	27	58.7	11	1 US-08-277-660A-4	Sequence 4, App1
11	27	58.7	11	1 US-08-277-660A-11	Sequence 42, App1
12	27	58.7	11	1 US-08-277-660A-12	Sequence 42, App1
13	27	58.7	11	1 US-08-277-660A-13	Sequence 9, App1
14	27	58.7	11	1 US-08-277-660A-19	Sequence 10, App1
15	27	58.7	11	1 US-08-277-660A-20	Sequence 11, App1
16	27	58.7	11	1 US-08-424-957-17	Sequence 12, App1
17	27	58.7	11	1 US-08-424-957-23	Sequence 13, App1
18	27	58.7	11	1 US-08-424-957-24	Sequence 19, App1
19	27	58.7	11	1 US-08-424-957-25	Sequence 20, App1
20	27	58.7	11	1 US-08-424-957-26	Sequence 17, App1
21	27	58.7	11	3 US-09-035-686-23	Sequence 23, App1
22	27	58.7	11	3 US-09-035-686-24	Sequence 24, App1
23	27	58.7	11	3 US-09-035-686-25	Sequence 25, App1
24	27	58.7	11	3 US-09-035-686-26	Sequence 26, App1
25	27	58.7	11	3 US-09-035-686-32	Sequence 32, App1
26	27	58.7	11	3 US-09-035-686-33	Sequence 33, App1
27	27	58.7	11	3 US-09-035-686-34	Sequence 34, App1

Query Match 65.2%; Score 30; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 4 FSELW 8

**ALIGNMENTS**

Db 5 FSELW 9

RESULT 2  
US-09-035-686-42  
; Sequence 42, Application US/09035686

GENERAL INFORMATION:  
APPLICANT: Picklesley, Steven M.  
PATENT NO. 6153391  
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/035, 686

APPLICATION NUMBER: US/09/035, 686

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/035, 686

PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/424, 957

FILING DATE: 19-APR-1995

APPLICATION NUMBER: US 08/277, 660

FILING DATE: 20-JUL-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REFERENCE/DOCKET NUMBER: 24, 190

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249

TELEFAX: 910 277-999

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear

US-08-277-6604-9

RESULT 4  
US-08-277-660A-10  
Sequence 10, Application US/08277660A  
Patent No. 5702008

GENERAL INFORMATION:  
APPLICANT: Bicksley, Steven M.  
APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277, 660A

APPLICATION NUMBER: US/08/277, 660A

ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REFERENCE/DOCKET NUMBER: 24, 190

TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249

TELEFAX: 910 277-999

INFORMATION FOR SEQ ID NO: 10:

QY 4 FSELW 8  
Db 5 FSDLW 9

QY 4 FSELW 8  
Db 5 FSDLW 9

QY 4 FSELW 8  
Db 5 FSELW 9

RESULT 3  
US-08-277-660A-9  
Sequence 9, Application US/08277660A  
Patent No. 5702008

GENERAL INFORMATION:  
APPLICANT: Picklesley, Steven M.  
APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400

SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear

US-08-277-660A-10

Query Match	58.7%	Score 27;	DB 1;	Length 11;
Best Local Similarity	80.0%	Pred. No. 64;		
Matches	4;	Mismatches 1;	Indels 0;	Gaps 0;

FY 4 FSELW 8  
 Db 5 FSDLW 9

RESULT 5  
 US-08-277-660A-11  
 Sequence 11, Application US/08277660A  
 Patent No. 5702908

GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 ATTORNEY/AGENT INFORMATION:  
 Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

CURRENT APPLICATION DATA:  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/277,660A  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-60244/WHD

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear

US-08-277-660A-12

RESULT 7  
 US-08-277-660A-13  
 Sequence 13, Application US/08277660A  
 Patent No. 5702908

GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 ATTORNEY/AGENT INFORMATION:  
 Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-60244/WHD

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear

US-08-277-660A-11

Query Match 58.7% Score 27; DB 1; Length 11;  
 Best Local Similarity 80.0% Pred. No. 64;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

FY 4 FSELW 8  
 Db 5 FSDLW 9

RESULT 6  
 US-08-277-660A-12  
 Sequence 12, Application US/08277660A  
 Patent No. 5702908

GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.

REGISTRATION NUMBER: 24,190  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEX: (415) 398-3249  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-277-660A-13

Query Match 58.7%; Score 27; DB 1; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 64;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSEIW 8  
 Db 5 FSDIW 9

---

RESULT 9  
 US-08-277-660A-19  
 Sequence 19, Application US/08277660A  
 Patent No. 5702908

GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277-660A  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-60244/WHD  
 TELECOMMUNICATION INFORMATION:  
 APPLICATION NUMBER: US/08/277-660A  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-60244/WHD  
 TELECOMMUNICATION INFORMATION:  
 APPLICATION NUMBER: US/08/277-660A  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.

RESULT 9  
 US-08-277-660A-20  
 Sequence 20, Application US/08277660A  
 Patent No. 5702908

GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277-660A  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.

RESULT 8  
 US-08-277-660A-19  
 Sequence 19, Application US/08277660A  
 Patent No. 5702908

GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277-660A  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.

RESULT 8  
 US-08-277-660A-20  
 Sequence 20, Application US/08277660A  
 Patent No. 5702908

GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277-660A  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.

RESULT 10  
 US-08-424-957-17  
 Sequence 17, Application US/08424957  
 Patent No. 5770377

GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424957  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.

RESULT 10  
 US-08-424-957-17  
 Sequence 17, Application US/08424957  
 Patent No. 5770377

GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424957  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.

Query Match 58.7%; Score 27; DB 1; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 64;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSEIW 8  
 Db 5 FSDIW 9

```

// SOFTWARE: PatentIn Release #1.0, Version #1.30
// CURRENT APPLICATION DATA:
// APPLICATION NUMBER: US/08/424, 957
// FILING DATE: 19-APR-1995
// CLASSIFICATION:
// PRIORITY APPLICATION DATA:
// APPLICATION NUMBER: US 08/277, 660
// FILING DATE: 20-JUL-1994
// ATTORNEY/AGENT INFORMATION:
// NAME: Dreger, Walter H.
// REGISTRATION NUMBER: 24,190
// REFERENCE/DOCKET NUMBER: A-6122B/WHD
// TELECOMMUNICATION INFORMATION:
// TELEPHONE: (415) 781-1989
// TELEX: 910 277299
// INFORMATION FOR SEQ ID NO: 17:
// SEQUENCE CHARACTERISTICS:
// LENGTH: 11 amino acids
// TYPE: amino acid
// STRANDEDNESS: unknown
// US-08-424-957-17

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSBLW 8
Db 5 FSDLW 9

RESULT 12
US-08-424-957-24
// Sequence 24, Application US/08424957
// Patent No. 5770377
// GENERAL INFORMATION:
// APPLICANT: Lane, David P.
// ATTORNEY: Lane, David P.
// TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
// TITLE OF INVENTION: Protein and Therapeutic Application Thereof
// NUMBER OF SEQUENCES: 50
// CORRESPONDENCE ADDRESS:
// ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
// STREET: Four Embarcadero Center, Suite 3400
// CITY: San Francisco
// STATE: California
// COUNTRY: United States
// ZIP: 94111-4187
// COMPUTER READABLE FORM:
// MEDIUM TYPE: Floppy disk
// COMPUTER: IBM PC compatible
// OPERATING SYSTEM: PC-DOS/MS-DOS
// SOFTWARE: PatentIn Release #1.0, Version #1.30
// CURRENT APPLICATION DATA:
// APPLICATION NUMBER: US/08/424, 957
// FILING DATE: 19-APR-1995
// CLASSIFICATION:
// PRIOR APPLICATION DATA:
// APPLICATION NUMBER: US 08/277, 660
// FILING DATE: 20-JUL-1994
// ATTORNEY/AGENT INFORMATION:
// NAME: Dreger, Walter H.
// REGISTRATION NUMBER: 24,190
// REFERENCE/DOCKET NUMBER: A-6122B/WHD
// TELECOMMUNICATION INFORMATION:
// TELEPHONE: (415) 781-1989
// TELEFAX: (415) 398-3249
// TELELEX: 910 277299
// INFORMATION FOR SEQ ID NO: 24:
// SEQUENCE CHARACTERISTICS:
// LENGTH: 11 amino acids
// TYPE: amino acid
// STRANDEDNESS: unknown
// TOPOLOGY: unknown
// US-08-424-957-24

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSBLW 8
Db 5 FSDLW 9

RESULT 13
US-08-424-957-25
// Sequence 25, Application US/08424957
// Patent No. 5770377
// GENERAL INFORMATION:
// 
```

APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fliehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,957  
 FILING DATE: 19-APR-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-08-424-957-25

Query Match 58.7%; Score 27; DB 1; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 64;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

---

RESULT 14  
 US-08-424-957-32  
 Sequence 32; Application US/08424957  
 Patent No. 5770377  
 GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fliehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 PHONE: (415) 781-1989  
 FAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-08-424-957-26

Query Match 58.7%; Score 27; DB 1; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 64;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

---

RESULT 14  
 US-08-424-957-26  
 Sequence 26; Application US/08424957  
 Patent No. 5770377  
 GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fliehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,957

**Tue Sep 21 08:51:50 2004**

**audet-seq1.szlm.rai**

**Page 7**

US-08-424-957-32

Query Match 58.7%; Score 27; DB 1; Length 11;  
Best Local Similarity 80.0%; Pred. No. 64;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8  
| : ||  
Db 5 FSDLW 9

Search completed: September 20, 2004, 17:32:33  
Job time : 18 secs

B  
I  
A  
N  
K

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2004, 17:28:40 ; Search time 36 Seconds  
(without alignments)  
70.115 Million cell updates/sec

Title: AUDET-SEQ1  
Perfect score: 46  
Sequence: 1 gsfFfSeIw 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315516202 residues

Total number of hits satisfying chosen parameters: 2511

Minimum DB seq length: 11  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:  
 1: sp\_archea:  
 2: sp\_bacteria:  
 3: sp\_fungi:  
 4: sp\_human:  
 5: sp\_invertebrate:  
 6: sp\_mammal:  
 7: sp\_mhc:  
 8: sp\_organelle:  
 9: sp\_phage:  
 10: sp\_plant:  
 11: sp\_rabbit:  
 12: sp\_virus:  
 13: sp\_vertebrate:  
 14: sp\_unclassified:  
 15: sp\_rvirus:  
 16: sp\_bacteriophage:  
 17: sp\_archaea:  
 18: sp\_archea:  
 19: sp\_bacteria:  
 20: sp\_fungi:  
 21: sp\_invertebrate:  
 22: sp\_mammal:  
 23: sp\_mhc:  
 24: sp\_organelle:  
 25: sp\_phage:  
 26: sp\_plant:  
 27: sp\_rabbit:  
 28: sp\_virus:  
 29: sp\_vertebrate:  
 30: sp\_unclassified:  
 31: sp\_rvirus:  
 32: sp\_bacteriophage:  
 33: sp\_archea:  
 34: sp\_bacteria:  
 35: sp\_fungi:  
 36: sp\_invertebrate:  
 37: sp\_mammal:  
 38: sp\_mhc:  
 39: sp\_organelle:  
 40: sp\_phage:  
 41: sp\_plant:  
 42: sp\_rabbit:  
 43: sp\_virus:  
 44: sp\_vertebrate:  
 45: sp\_unclassified:  
 46: sp\_rvirus:  
 47: sp\_bacteriophage:  
 48: sp\_archea:  
 49: sp\_bacteria:  
 50: sp\_fungi:  
 51: sp\_invertebrate:  
 52: sp\_mammal:  
 53: sp\_mhc:  
 54: sp\_organelle:  
 55: sp\_phage:  
 56: sp\_plant:  
 57: sp\_rabbit:  
 58: sp\_virus:  
 59: sp\_vertebrate:  
 60: sp\_unclassified:  
 61: sp\_rvirus:  
 62: sp\_bacteriophage:  
 63: sp\_archea:  
 64: sp\_bacteria:  
 65: sp\_fungi:  
 66: sp\_invertebrate:  
 67: sp\_mammal:  
 68: sp\_mhc:  
 69: sp\_organelle:  
 70: sp\_phage:  
 71: sp\_plant:  
 72: sp\_rabbit:  
 73: sp\_virus:  
 74: sp\_vertebrate:  
 75: sp\_unclassified:  
 76: sp\_rvirus:  
 77: sp\_bacteriophage:  
 78: sp\_archea:  
 79: sp\_bacteria:  
 80: sp\_fungi:  
 81: sp\_invertebrate:  
 82: sp\_mammal:  
 83: sp\_mhc:  
 84: sp\_organelle:  
 85: sp\_phage:  
 86: sp\_plant:  
 87: sp\_rabbit:  
 88: sp\_virus:  
 89: sp\_vertebrate:  
 90: sp\_unclassified:  
 91: sp\_rvirus:  
 92: sp\_bacteriophage:  
 93: sp\_archea:  
 94: sp\_bacteria:  
 95: sp\_fungi:  
 96: sp\_invertebrate:  
 97: sp\_mammal:  
 98: sp\_mhc:  
 99: sp\_organelle:  
 100: sp\_phage:  
 101: sp\_plant:  
 102: sp\_rabbit:  
 103: sp\_virus:  
 104: sp\_vertebrate:  
 105: sp\_unclassified:  
 106: sp\_rvirus:  
 107: sp\_bacteriophage:  
 108: sp\_archea:  
 109: sp\_bacteria:  
 110: sp\_fungi:  
 111: sp\_invertebrate:  
 112: sp\_mammal:  
 113: sp\_mhc:  
 114: sp\_organelle:  
 115: sp\_phage:  
 116: sp\_plant:  
 117: sp\_rabbit:  
 118: sp\_virus:  
 119: sp\_vertebrate:  
 120: sp\_unclassified:  
 121: sp\_rvirus:  
 122: sp\_bacteriophage:  
 123: sp\_archea:  
 124: sp\_bacteria:  
 125: sp\_fungi:  
 126: sp\_invertebrate:  
 127: sp\_mammal:  
 128: sp\_mhc:  
 129: sp\_organelle:  
 130: sp\_phage:  
 131: sp\_plant:  
 132: sp\_rabbit:  
 133: sp\_virus:  
 134: sp\_vertebrate:  
 135: sp\_unclassified:  
 136: sp\_rvirus:  
 137: sp\_bacteriophage:  
 138: sp\_archea:  
 139: sp\_bacteria:  
 140: sp\_fungi:  
 141: sp\_invertebrate:  
 142: sp\_mammal:  
 143: sp\_mhc:  
 144: sp\_organelle:  
 145: sp\_phage:  
 146: sp\_plant:  
 147: sp\_rabbit:  
 148: sp\_virus:  
 149: sp\_vertebrate:  
 150: sp\_unclassified:  
 151: sp\_rvirus:  
 152: sp\_bacteriophage:  
 153: sp\_archea:  
 154: sp\_bacteria:  
 155: sp\_fungi:  
 156: sp\_invertebrate:  
 157: sp\_mammal:  
 158: sp\_mhc:  
 159: sp\_organelle:  
 160: sp\_phage:  
 161: sp\_plant:  
 162: sp\_rabbit:  
 163: sp\_virus:  
 164: sp\_vertebrate:  
 165: sp\_unclassified:  
 166: sp\_rvirus:  
 167: sp\_bacteriophage:  
 168: sp\_archea:  
 169: sp\_bacteria:  
 170: sp\_fungi:  
 171: sp\_invertebrate:  
 172: sp\_mammal:  
 173: sp\_mhc:  
 174: sp\_organelle:  
 175: sp\_phage:  
 176: sp\_plant:  
 177: sp\_rabbit:  
 178: sp\_virus:  
 179: sp\_vertebrate:  
 180: sp\_unclassified:  
 181: sp\_rvirus:  
 182: sp\_bacteriophage:  
 183: sp\_archea:  
 184: sp\_bacteria:  
 185: sp\_fungi:  
 186: sp\_invertebrate:  
 187: sp\_mammal:  
 188: sp\_mhc:  
 189: sp\_organelle:  
 190: sp\_phage:  
 191: sp\_plant:  
 192: sp\_rabbit:  
 193: sp\_virus:  
 194: sp\_vertebrate:  
 195: sp\_unclassified:  
 196: sp\_rvirus:  
 197: sp\_bacteriophage:  
 198: sp\_archea:  
 199: sp\_bacteria:  
 200: sp\_fungi:  
 201: sp\_invertebrate:  
 202: sp\_mammal:  
 203: sp\_mhc:  
 204: sp\_organelle:  
 205: sp\_phage:  
 206: sp\_plant:  
 207: sp\_rabbit:  
 208: sp\_virus:  
 209: sp\_vertebrate:  
 210: sp\_unclassified:  
 211: sp\_rvirus:  
 212: sp\_bacteriophage:  
 213: sp\_archea:  
 214: sp\_bacteria:  
 215: sp\_fungi:  
 216: sp\_invertebrate:  
 217: sp\_mammal:  
 218: sp\_mhc:  
 219: sp\_organelle:  
 220: sp\_phage:  
 221: sp\_plant:  
 222: sp\_rabbit:  
 223: sp\_virus:  
 224: sp\_vertebrate:  
 225: sp\_unclassified:  
 226: sp\_rvirus:  
 227: sp\_bacteriophage:  
 228: sp\_archea:  
 229: sp\_bacteria:  
 230: sp\_fungi:  
 231: sp\_invertebrate:  
 232: sp\_mammal:  
 233: sp\_mhc:  
 234: sp\_organelle:  
 235: sp\_phage:  
 236: sp\_plant:  
 237: sp\_rabbit:  
 238: sp\_virus:  
 239: sp\_vertebrate:  
 240: sp\_unclassified:  
 241: sp\_rvirus:  
 242: sp\_bacteriophage:  
 243: sp\_archea:  
 244: sp\_bacteria:  
 245: sp\_fungi:  
 246: sp\_invertebrate:  
 247: sp\_mammal:  
 248: sp\_mhc:  
 249: sp\_organelle:  
 250: sp\_phage:  
 251: sp\_plant:  
 252: sp\_rabbit:  
 253: sp\_virus:  
 254: sp\_vertebrate:  
 255: sp\_unclassified:  
 256: sp\_rvirus:  
 257: sp\_bacteriophage:  
 258: sp\_archea:  
 259: sp\_bacteria:  
 260: sp\_fungi:  
 261: sp\_invertebrate:  
 262: sp\_mammal:  
 263: sp\_mhc:  
 264: sp\_organelle:  
 265: sp\_phage:  
 266: sp\_plant:  
 267: sp\_rabbit:  
 268: sp\_virus:  
 269: sp\_vertebrate:  
 270: sp\_unclassified:  
 271: sp\_rvirus:  
 272: sp\_bacteriophage:  
 273: sp\_archea:  
 274: sp\_bacteria:  
 275: sp\_fungi:  
 276: sp\_invertebrate:  
 277: sp\_mammal:  
 278: sp\_mhc:  
 279: sp\_organelle:  
 280: sp\_phage:  
 281: sp\_plant:  
 282: sp\_rabbit:  
 283: sp\_virus:  
 284: sp\_vertebrate:  
 285: sp\_unclassified:  
 286: sp\_rvirus:  
 287: sp\_bacteriophage:  
 288: sp\_archea:  
 289: sp\_bacteria:  
 290: sp\_fungi:  
 291: sp\_invertebrate:  
 292: sp\_mammal:  
 293: sp\_mhc:  
 294: sp\_organelle:  
 295: sp\_phage:  
 296: sp\_plant:  
 297: sp\_rabbit:  
 298: sp\_virus:  
 299: sp\_vertebrate:  
 300: sp\_unclassified:  
 301: sp\_rvirus:  
 302: sp\_bacteriophage:  
 303: sp\_archea:  
 304: sp\_bacteria:  
 305: sp\_fungi:  
 306: sp\_invertebrate:  
 307: sp\_mammal:  
 308: sp\_mhc:  
 309: sp\_organelle:  
 310: sp\_phage:  
 311: sp\_plant:  
 312: sp\_rabbit:  
 313: sp\_virus:  
 314: sp\_vertebrate:  
 315: sp\_unclassified:  
 316: sp\_rvirus:  
 317: sp\_bacteriophage:  
 318: sp\_archea:  
 319: sp\_bacteria:  
 320: sp\_fungi:  
 321: sp\_invertebrate:  
 322: sp\_mammal:  
 323: sp\_mhc:  
 324: sp\_organelle:  
 325: sp\_phage:  
 326: sp\_plant:  
 327: sp\_rabbit:  
 328: sp\_virus:  
 329: sp\_vertebrate:  
 330: sp\_unclassified:  
 331: sp\_rvirus:  
 332: sp\_bacteriophage:  
 333: sp\_archea:  
 334: sp\_bacteria:  
 335: sp\_fungi:  
 336: sp\_invertebrate:  
 337: sp\_mammal:  
 338: sp\_mhc:  
 339: sp\_organelle:  
 340: sp\_phage:  
 341: sp\_plant:  
 342: sp\_rabbit:  
 343: sp\_virus:  
 344: sp\_vertebrate:  
 345: sp\_unclassified:  
 346: sp\_rvirus:  
 347: sp\_bacteriophage:  
 348: sp\_archea:  
 349: sp\_bacteria:  
 350: sp\_fungi:  
 351: sp\_invertebrate:  
 352: sp\_mammal:  
 353: sp\_mhc:  
 354: sp\_organelle:  
 355: sp\_phage:  
 356: sp\_plant:  
 357: sp\_rabbit:  
 358: sp\_virus:  
 359: sp\_vertebrate:  
 360: sp\_unclassified:  
 361: sp\_rvirus:  
 362: sp\_bacteriophage:  
 363: sp\_archea:  
 364: sp\_bacteria:  
 365: sp\_fungi:  
 366: sp\_invertebrate:  
 367: sp\_mammal:  
 368: sp\_mhc:  
 369: sp\_organelle:  
 370: sp\_phage:  
 371: sp\_plant:  
 372: sp\_rabbit:  
 373: sp\_virus:  
 374: sp\_vertebrate:  
 375: sp\_unclassified:  
 376: sp\_rvirus:  
 377: sp\_bacteriophage:  
 378: sp\_archea:  
 379: sp\_bacteria:  
 380: sp\_fungi:  
 381: sp\_invertebrate:  
 382: sp\_mammal:  
 383: sp\_mhc:  
 384: sp\_organelle:  
 385: sp\_phage:  
 386: sp\_plant:  
 387: sp\_rabbit:  
 388: sp\_virus:  
 389: sp\_vertebrate:  
 390: sp\_unclassified:  
 391: sp\_rvirus:  
 392: sp\_bacteriophage:  
 393: sp\_archea:  
 394: sp\_bacteria:  
 395: sp\_fungi:  
 396: sp\_invertebrate:  
 397: sp\_mammal:  
 398: sp\_mhc:  
 399: sp\_organelle:  
 400: sp\_phage:  
 401: sp\_plant:  
 402: sp\_rabbit:  
 403: sp\_virus:  
 404: sp\_vertebrate:  
 405: sp\_unclassified:  
 406: sp\_rvirus:  
 407: sp\_bacteriophage:  
 408: sp\_archea:  
 409: sp\_bacteria:  
 410: sp\_fungi:  
 411: sp\_invertebrate:  
 412: sp\_mammal:  
 413: sp\_mhc:  
 414: sp\_organelle:  
 415: sp\_phage:  
 416: sp\_plant:  
 417: sp\_rabbit:  
 418: sp\_virus:  
 419: sp\_vertebrate:  
 420: sp\_unclassified:  
 421: sp\_rvirus:  
 422: sp\_bacteriophage:  
 423: sp\_archea:  
 424: sp\_bacteria:  
 425: sp\_fungi:  
 426: sp\_invertebrate:  
 427: sp\_mammal:  
 428: sp\_mhc:  
 429: sp\_organelle:  
 430: sp\_phage:  
 431: sp\_plant:  
 432: sp\_rabbit:  
 433: sp\_virus:  
 434: sp\_vertebrate:  
 435: sp\_unclassified:  
 436: sp\_rvirus:  
 437: sp\_bacteriophage:  
 438: sp\_archea:  
 439: sp\_bacteria:  
 440: sp\_fungi:  
 441: sp\_invertebrate:  
 442: sp\_mammal:  
 443: sp\_mhc:  
 444: sp\_organelle:  
 445: sp\_phage:  
 446: sp\_plant:  
 447: sp\_rabbit:  
 448: sp\_virus:  
 449: sp\_vertebrate:  
 450: sp\_unclassified:  
 451: sp\_rvirus:  
 452: sp\_bacteriophage:  
 453: sp\_archea:  
 454: sp\_bacteria:  
 455: sp\_fungi:  
 456: sp\_invertebrate:  
 457: sp\_mammal:  
 458: sp\_mhc:  
 459: sp\_organelle:  
 460: sp\_phage:  
 461: sp\_plant:  
 462: sp\_rabbit:  
 463: sp\_virus:  
 464: sp\_vertebrate:  
 465: sp\_unclassified:  
 466: sp\_rvirus:  
 467: sp\_bacteriophage:  
 468: sp\_archea:  
 469: sp\_bacteria:  
 470: sp\_fungi:  
 471: sp\_invertebrate:  
 472: sp\_mammal:  
 473: sp\_mhc:  
 474: sp\_organelle:  
 475: sp\_phage:  
 476: sp\_plant:  
 477: sp\_rabbit:  
 478: sp\_virus:  
 479: sp\_vertebrate:  
 480: sp\_unclassified:  
 481: sp\_rvirus:  
 482: sp\_bacteriophage:  
 483: sp\_archea:  
 484: sp\_bacteria:  
 485: sp\_fungi:  
 486: sp\_invertebrate:  
 487: sp\_mammal:  
 488: sp\_mhc:  
 489: sp\_organelle:  
 490: sp\_phage:  
 491: sp\_plant:  
 492: sp\_rabbit:  
 493: sp\_virus:  
 494: sp\_vertebrate:  
 495: sp\_unclassified:  
 496: sp\_rvirus:  
 497: sp\_bacteriophage:  
 498: sp\_archea:  
 499: sp\_bacteria:  
 500: sp\_fungi:  
 501: sp\_invertebrate:  
 502: sp\_mammal:  
 503: sp\_mhc:  
 504: sp\_organelle:  
 505: sp\_phage:  
 506: sp\_plant:  
 507: sp\_rabbit:  
 508: sp\_virus:  
 509: sp\_vertebrate:  
 510: sp\_unclassified:  
 511: sp\_rvirus:  
 512: sp\_bacteriophage:  
 513: sp\_archea:  
 514: sp\_bacteria:  
 515: sp\_fungi:  
 516: sp\_invertebrate:  
 517: sp\_mammal:  
 518: sp\_mhc:  
 519: sp\_organelle:  
 520: sp\_phage:  
 521: sp\_plant:  
 522: sp\_rabbit:  
 523: sp\_virus:  
 524: sp\_vertebrate:  
 525: sp\_unclassified:  
 526: sp\_rvirus:  
 527: sp\_bacteriophage:  
 528: sp\_archea:  
 529: sp\_bacteria:  
 530: sp\_fungi:  
 531: sp\_invertebrate:  
 532: sp\_mammal:  
 533: sp\_mhc:  
 534: sp\_organelle:  
 535: sp\_phage:  
 536: sp\_plant:  
 537: sp\_rabbit:  
 538: sp\_virus:  
 539: sp\_vertebrate:  
 540: sp\_unclassified:  
 541: sp\_rvirus:  
 542: sp\_bacteriophage:  
 543: sp\_archea:  
 544: sp\_bacteria:  
 545: sp\_fungi:  
 546: sp\_invertebrate:  
 547: sp\_mammal:  
 548: sp\_mhc:  
 549: sp\_organelle:  
 550: sp\_phage:  
 551: sp\_plant:  
 552: sp\_rabbit:  
 553: sp\_virus:  
 554: sp\_vertebrate:  
 555: sp\_unclassified:  
 556: sp\_rvirus:  
 557: sp\_bacteriophage:  
 558: sp\_archea:  
 559: sp\_bacteria:  
 560: sp\_fungi:  
 561: sp\_invertebrate:  
 562: sp\_mammal:  
 563: sp\_mhc:  
 564: sp\_organelle:  
 565: sp\_phage:  
 566: sp\_plant:  
 567: sp\_rabbit:  
 568: sp\_virus:  
 569: sp\_vertebrate:  
 570: sp\_unclassified:  
 571: sp\_rvirus:  
 572: sp\_bacteriophage:  
 573: sp\_archea:  
 574: sp\_bacteria:  
 575: sp\_fungi:  
 576: sp\_invertebrate:  
 577: sp\_mammal:  
 578: sp\_mhc:  
 579: sp\_organelle:  
 580: sp\_phage:  
 581: sp\_plant:  
 582: sp\_rabbit:  
 583: sp\_virus:  
 584: sp\_vertebrate:  
 585: sp\_unclassified:  
 586: sp\_rvirus:  
 587: sp\_bacteriophage:  
 588: sp\_archea:  
 589: sp\_bacteria:  
 590: sp\_fungi:  
 591: sp\_invertebrate:  
 592: sp\_mammal:  
 593: sp\_mhc:  
 594: sp\_organelle:  
 595: sp\_phage:  
 596: sp\_plant:  
 597: sp\_rabbit:  
 598: sp\_virus:  
 599: sp\_vertebrate:  
 600: sp\_unclassified:  
 601: sp\_rvirus:  
 602: sp\_bacteriophage:  
 603: sp\_archea:  
 604: sp\_bacteria:  
 605: sp\_fungi:  
 606: sp\_invertebrate:  
 607: sp\_mammal:  
 608: sp\_mhc:  
 609: sp\_organelle:  
 610: sp\_phage:  
 611: sp\_plant:  
 612: sp\_rabbit:  
 613: sp\_virus:  
 614: sp\_vertebrate:  
 615: sp\_unclassified:  
 616: sp\_rvirus:  
 617: sp\_bacteriophage:  
 618: sp\_archea:  
 619: sp\_bacteria:  
 620: sp\_fungi:  
 621: sp\_invertebrate:  
 622: sp\_mammal:  
 623: sp\_mhc:  
 624: sp\_organelle:  
 625: sp\_phage:  
 626: sp\_plant:  
 627: sp\_rabbit:  
 628: sp\_virus:  
 629: sp\_vertebrate:  
 630: sp\_unclassified:  
 631: sp\_rvirus:  
 632: sp\_bacteriophage:  
 633: sp\_archea:  
 634: sp\_bacteria:  
 635: sp\_fungi:  
 636: sp\_invertebrate:  
 637: sp\_mammal:  
 638: sp\_mhc:  
 639: sp\_organelle:  
 640: sp\_phage:  
 641: sp\_plant:  
 642: sp\_rabbit:  
 643: sp\_virus:  
 644: sp\_vertebrate:  
 645: sp\_unclassified:  
 646: sp\_rvirus:  
 647: sp\_bacteriophage:  
 648: sp\_archea:  
 649: sp\_bacteria:  
 650: sp\_fungi:  
 651: sp\_invertebrate:  
 652: sp\_mammal:  
 653: sp\_mhc:  
 654: sp\_organelle:  
 655: sp\_phage:  
 656: sp\_plant:  
 657: sp\_rabbit:  
 658: sp\_virus:  
 659: sp\_vertebrate:  
 660: sp\_unclassified:  
 661: sp\_rvirus:  
 662: sp\_bacteriophage:  
 663: sp\_archea:  
 664: sp\_bacteria:  
 665: sp\_fungi:  
 666: sp\_invertebrate:  
 667: sp\_mammal:  
 668: sp\_mhc:  
 669: sp\_organelle:  
 670: sp\_phage:  
 671: sp\_plant:  
 672: sp\_rabbit:  
 673: sp\_virus:  
 674: sp\_vertebrate:  
 675: sp\_unclassified:  
 676: sp\_rvirus:  
 677: sp\_bacteriophage:  
 678: sp\_archea:  
 679: sp\_bacteria:  
 680: sp\_fungi:  
 681: sp\_invertebrate:  
 682: sp\_mammal:  
 683: sp\_mhc:  
 684: sp\_organelle:  
 685: sp\_phage:  
 686: sp\_plant:  
 687: sp\_rabbit:  
 688: sp\_virus:  
 689: sp\_vertebrate:  
 690: sp\_unclassified:  
 691: sp\_rvirus:  
 692: sp\_bacteriophage:  
 693: sp\_archea:  
 694: sp\_bacteria:  
 695: sp\_fungi:  
 696: sp\_invertebrate:  
 697: sp\_mammal:  
 698: sp\_mhc:  
 699: sp\_organelle:  
 700: sp\_phage:  
 701: sp\_plant:  
 702: sp\_rabbit:  
 703: sp\_virus:  
 704: sp\_vertebrate:  
 705: sp\_unclassified:  
 706: sp\_rvirus:  
 707: sp\_bacteriophage:  
 708: sp\_archea:  
 709: sp\_bacteria:  
 710: sp\_fungi:  
 711: sp\_invertebrate:  
 712: sp\_mammal:  
 713: sp\_mhc:  
 714: sp\_organelle:  
 715: sp\_phage:  
 716: sp\_plant:  
 717: sp\_rabbit:  
 718: sp\_virus:  
 719: sp\_vertebrate:  
 720: sp\_unclassified:  
 721: sp\_rvirus:  
 722: sp\_bacteriophage:  
 723: sp\_archea:  
 724: sp\_bacteria:  
 725: sp\_fungi:  
 726: sp\_invertebrate:  
 727: sp\_mammal:  
 728: sp\_mhc:  
 729: sp\_organelle:  
 730: sp\_phage:  
 731: sp\_plant:  
 732: sp\_rabbit:  
 733: sp\_virus:  
 734: sp\_vertebrate:  
 735: sp\_unclassified:  
 736: sp\_rvirus:  
 737: sp\_bacteriophage:  
 738: sp\_archea:  
 739: sp\_bacteria:  
 740: sp\_fungi:  
 741: sp\_invertebrate:  
 742: sp\_mammal:  
 743: sp\_mhc:  
 744: sp\_organelle:  
 745: sp\_phage:  
 746: sp\_plant:  
 747: sp\_rabbit:  
 748: sp\_virus:  
 749: sp\_vertebrate:  
 750: sp\_unclassified:  
 751: sp\_rvirus:  
 752: sp\_bacteriophage:  
 753: sp\_archea:  
 754: sp\_bacteria:  
 755: sp\_fungi:  
 756: sp\_invertebrate:  
 757: sp\_mammal:  
 758: sp\_mhc:  
 759: sp\_organelle:  
 760: sp\_phage:  
 761: sp\_plant:  
 762: sp\_rabbit:  
 763: sp\_virus:  
 764: sp\_vertebrate:  
 765: sp\_unclassified:  
 766: sp\_rvirus:  
 767: sp\_bacteriophage:  
 768: sp\_archea:  
 769: sp\_bacteria:  
 770: sp\_fungi:  
 771: sp\_invertebrate:  
 772: sp\_mammal:  
 773: sp\_mhc:  
 774: sp\_organelle:  
 775: sp\_phage:  
 776: sp\_plant:  
 777: sp\_rabbit:  
 778: sp\_virus:  
 779: sp\_vertebrate:  
 780: sp\_unclassified:  
 781: sp\_rvirus:  
 782: sp\_bacteriophage:  
 783: sp\_archea:  
 784: sp\_bacteria:  
 785: sp\_fungi:  
 786: sp\_invertebrate:  
 787: sp\_mammal:  
 788: sp\_mhc:  
 789: sp\_organelle:  
 790: sp\_phage:  
 791: sp\_plant:  
 792: sp\_rabbit:  
 793: sp\_virus:  
 794: sp\_vertebrate:  
 795: sp\_unclassified:  
 796: sp\_rvirus:  
 797: sp\_bacteriophage:  
 798: sp\_archea:  
 799: sp\_bacteria:  
 800: sp\_fungi:  
 801: sp\_invertebrate:  
 802: sp\_mammal:  
 803: sp\_mhc:  
 804: sp\_organelle:  
 805: sp\_phage:  
 806: sp\_plant:  
 807: sp\_rabbit:  
 808: sp\_virus:  
 809: sp\_vertebrate:  
 810: sp\_unclassified:  
 811: sp\_rvirus:  
 812: sp\_bacteriophage:  
 813: sp\_archea:  
 814: sp\_bacteria:  
 815: sp\_fungi:  
 816: sp\_invertebrate:  
 817: sp\_mammal:  
 818: sp\_mhc:  
 819: sp\_organelle:  
 820: sp\_phage:  
 821: sp\_plant:  
 822: sp\_rabbit:  
 823: sp\_virus:  
 824: sp\_vertebrate:  
 825: sp\_unclassified:  
 826: sp\_rvirus:  
 827: sp\_bacteriophage:  
 828: sp\_archea:  
 829: sp\_bacteria:  
 830: sp\_fungi:  
 831: sp\_invertebrate:  
 832: sp\_mammal:  
 833: sp\_mhc:  
 834: sp\_organelle:  
 835: sp\_phage:  
 836: sp\_plant:  
 837: sp\_rabbit:  
 838: sp\_virus:  
 839: sp\_vertebrate:  
 840: sp\_unclassified:  
 841: sp\_rvirus:  
 842: sp\_bacteriophage:  
 843: sp\_archea:  
 844: sp\_bacteria:  
 845: sp\_fungi:  
 846: sp\_invertebrate:  
 847: sp\_mammal:  
 848: sp\_mhc:  
 849: sp\_organelle:  
 850: sp\_phage:  
 851: sp\_plant:  
 852: sp\_rabbit:  
 853: sp\_virus:  
 854: sp\_vertebrate:  
 855: sp\_unclassified:  
 856: sp\_rvirus:  
 857: sp\_bacteriophage:  
 858: sp\_archea:  
 859: sp\_bacteria:  
 860: sp\_fungi:  
 861: sp\_invertebrate:  
 862: sp\_mammal:  
 863: sp\_mhc:  
 864: sp\_organelle:  
 865: sp\_phage:  
 866: sp\_plant:  
 867: sp\_rabbit:  
 868: sp\_virus:  
 869: sp\_vertebrate:  
 870: sp\_unclassified:  
 871: sp\_rvirus:  
 872: sp\_bacteriophage:  
 873: sp\_archea:  
 874: sp\_bacteria:  
 875: sp\_fungi:  
 876: sp\_invertebrate:  
 877: sp\_mammal:  
 878: sp\_mhc:  
 879: sp\_organelle:  
 880: sp\_phage:  
 881: sp\_plant:  
 882: sp\_rabbit:  
 883: sp\_virus:  
 884: sp\_vertebrate:

AC P83537; (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DT Unknown protein from 2D-page (Fragment).  
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=1625;  
RN [1] SEQUENCE, AND INDUCTION.  
RP STRAIN=DSM 2045;  
RC Published=12:12866;  
RX RT "High Pressure effects step-wise altered protein expression in  
Lactobacillus sanfranciscensis.";  
RT Proteomics 2:765-774 (2002).  
RL -1- INDUCTION: BY ELEVATED HYDROSTATIC PRESSURE.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN  
PROTEIN IS: 65 kDa.  
FT NON\_TER 1  
FT 11 AA; 11 MW; D96C8231B771ADD9 CRC64;  
SQ SEQUENCE 11 AA; 1249 MW;

Query Match Score 23; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFS 5  
Db 1 GSFFA 5

---

RESULT 3  
ID Q77895 PRELIMINARY; PRT; 11 AA.  
AC Q77895; (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
MHC class II B locus 12 (Fragment).  
OS Oreochromis niloticus (Nile tilapia).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Osteichthyes; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Osteichthyes; Acanthopterygii; Percormorpha; Perciformes; Labroidei;  
Cichlidae; Oreochromis.  
NCBI\_TaxID=8128;

RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo B.; Zaleska-Rutczynska Z.; McAndrew B.; Vincek V.,  
Figueroa F.; Sulmann H.; Klein J.; Klein J.;  
RT "Linkage relationships and haplotypes polymorphism among cichlid mhc  
class II B loci.";  
RT Genetics 149:1527-1537 (1998).  
EMBL; AF050005; AAC41344.1; -.  
FT NON\_TER 1  
FT 11 AA; 11 MW; 1367 MW;

SQ SEQUENCE 11 AA; 1367 MW;

Query Match Score 23; DB 7; Length 11;  
Best Local Similarity 50.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

---

RESULT 4  
ID Q9XLI2 PRELIMINARY; PRT; 13 AA.  
Db 3 FFWSTLW 8

---

RESULT 5  
ID Q9RSD6 PRELIMINARY; PRT; 15 AA.  
AC Q9RSD6; (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 13, Last annotation update)

DT 01-MAY-2000 (TREMBLrel. 14, Last sequence update)  
DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 41 kDa protein  
(Fragment).  
OS Chromatium vinosum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;  
OC Chromataceae; Allochromatium.  
NCBI\_TaxID=1049;

RN [1] SEQUENCE  
RP MEDLINE=93146381; PubMed=1490603;  
RA Liebergesell M.; Schmidt B.; Steinbuchel A.;  
RT "Isolation and identification of gramine-associated proteins relevant  
for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum  
D.,"  
RL FEMS Microbiol. Lett. 78:227-232 (1992).  
SQ SEQUENCE 15 AA; 1874 MW; 165P9A16BCA2A9D CRC64;

Query Match Score 23; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 9.7e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SFFSEELW 8  
Db 5 NFFDDW 11

---

RESULT 6  
ID Q9RT7 PRELIMINARY; PRT; 12 AA.  
AC Q9RT7; (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE 15-kDa amyloid protein A homolog (Fragment).

OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 [1] NCBI\_TaxID=9913;  
 RN SEQUENCE.  
 RX MEDLINE=92132498; PubMed=1734497;  
 RA Veiby O P.; Sletten K.; Husby G.; Nordstoga K.;  
 RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils  
 of bovine kidney.";  
 Scand. J. Immunol. 35:63-69(1992).  
 RL NON\_TER 1 1  
 FT NON\_TER 12 12  
 SEQUENCE 12 AA; 1503 MW; 64CDB543C6D84AEB CRC64;  
 Query Match Similarity 47.8%; Score 22; DB 6; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 SFPSSELW 8  
 Db 1 SFPEXEXY 7

RESULT 7  
 ID 077898 PRELIMINARY; PRT; 11 AA.  
 AC 077898; Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 12 (Fragment).  
 DE Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OS Oreochromis niloticus (Nile tilapia).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Neopterygii; Perciformes; Labroidei;  
 OC Acanthopterygii; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OC NCBI\_TaxID=8128;

RN SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E.; Zaleska-Rutczynska Z.; McAndrew B.; Vinczek V.;  
 RA Figueiroa F.; Sultmann H.; Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 class II B loci.";  
 Genetics 149:1527-1537(1998).  
 RL NON\_TER 1 1  
 FT NON\_TER 11 11  
 SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;  
 Query Match Similarity 43.5%; Score 20; DB 7; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 3 FFSELW 8  
 Db 3 FWSIVW 8

RESULT 8  
 ID 077894 PRELIMINARY; PRT; 11 AA.  
 AC 077894; Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 12 (Fragment).  
 DE Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OS Oreochromis niloticus (Nile tilapia).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidei;

OC NCBI\_TaxID=96667;

RN SEQUENCE FROM N.A.  
 RX MEDLINE=9724585; PubMed=9060417;  
 RA Loebel D.A.; Johnston P.G.;  
 RT "Analysis of the intron-exon structure of the G6PD gene of the  
 wallaroo (Macropus robustus) by polymerase chain reaction.";  
 RL Genome 8:146-147(1997).  
 DR U53774; AAC48789.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 12 12  
 SEQUENCE 12 AA; 1430 MW; D42A9CB4E3CB1AA9 CRC64;  
 Query Match Similarity 43.5%; Score 20; DB 6; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSFFPE 6  
 Db 2 GGYFDB 7

RESULT 9  
 ID 046664 PRELIMINARY; PRT; 12 AA.  
 AC 046664; Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Glucose-6-phosphate dehydrogenase (Fragment).  
 DE G6PD.  
 OS Macropus robustus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
 OC NCBI\_TaxID=25580;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=9724585; PubMed=9060417;  
 RA Loebel D.A.; Johnston P.G.;  
 RT "Analysis of the intron-exon structure of the G6PD gene of the  
 wallaroo (Macropus robustus) by polymerase chain reaction.";  
 RL Genome 8:146-147(1997).  
 DR U53774; AAC48789.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 12 12  
 SEQUENCE 12 AA; 1430 MW; D42A9CB4E3CB1AA9 CRC64;  
 Query Match Similarity 43.5%; Score 20; DB 6; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSFFPE 6  
 Db 2 GGYFDB 7

RESULT 10  
 ID Q9UC46 PRELIMINARY; PRT; 11 AA.  
 AC Q9UC46; Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Neutrophil inhibitor peptide, NIP-POLYMORPHONUCLEAR neutrophil  
 DE inhibitor peptide.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OC NCBI\_TaxID=96667;  
 RN [1] NCBI\_TaxID=8128;  
 RP SEQUENCE.

Query Match 41.3%; Score 19; DB 4; Length 11;  
Best Local Similarity 75.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSFF 4  
Db 3 GSYF 6

---

RESULT 11  
ID Q53579 PRELIMINARY; PRT; 12 AA.  
AC Q53579;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DB Light-harvesting complex I alpha polypeptide (Fragment).  
GN pufA.  
OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).  
OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92234363; PubMed=1563029;  
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufA mutants".  
RT J. Bacteriol. 174:3030-3041(1992).  
DR EMBL; S97551; AAC60405.1;  
FT NON TER 12 12  
SEQUENCE 12 AA; 1627 MW; 0F92F6EA8A70532B CRC64;  
SQ

Query Match 41.3%; Score 19; DB 2; Length 12;  
Best Local Similarity 42.9%; Pred. No. 5e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFFSEIWF 8  
Db 2 SKFYKIKW 8

---

RESULT 12  
ID Q812E2 PRELIMINARY; PRT; 13 AA.  
AC Q812E2;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DE Hypothetical protein (Fragment).  
GN PFA0655W.  
OS Plasmodium falciparum (isolate 3D7).  
OC Bukaryote; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22255708; PubMed=12368867;  
RA Hall N.; Pain A.; Beriman M.; Churcher C.; Harris B.; Harris D.;  
RA Mungall K.; Bowman S.; Atkin R.; Baker S.; Barron A.; Brooks K.;  
RA Buckee C.O.; Burrows C.; Cherevach I.; Chillingworth C.;  
RA Cronin A.; Davies R.; Davis P.; Dear P.; Dearden F.; Doggett J.;  
RA Feltwell T.; Goble A.; Goodhead I.; Gwilliam R.; Hamlin N.; Hance Z.;  
RA Harper D.; Hauser H.; Hornsby T.; Holroyd S.; Horrocks P.;

RA Humphrey S.; Jagels K.; James K.D.; Johnson D.; Kerhoornou A.;  
RA Knights A.; Konforov B.; Kyes S.; Larke N.; Lawson D.; Leonard N.;  
RA Line A.; Macdonald M.; McLean J.; Mooney P.; Moule S.; Murphy L.;  
RA Oliver K.; Ormond D.; Price C.; Quail M.A.; Rabbinowitch E.;  
RA Rajandream M.A.; Rutter S.; Rutherford K.M.; Sanders M.; Simmonds M.;  
RA Seeger K.; Sharp S.; Smith R.; Squares R.; Stevens K.;  
RA Taylor K.; Tivey A.; Unwin L.; Whitehead S.; Woodward J.;  
RA Sulston J.E.; Craig A.; Newbold C.; Barrell B.G.;  
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";  
RL Nature 411:527-531(2002).  
DR EMBL; AL031744; Cap48947.1; -.  
KW Hypothetical protein.  
FT NON TER 1 1  
SQ SEQUENCE 13 AA; 1619 MW; 50E352E2F7FED1A7 CRC64;

Query Match 41.3%; Score 19; DB 5; Length 13;  
Best Local Similarity 60.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SFFSEIWF 6  
Db 7 TFYSE 11

---

RESULT 13  
ID Q47832 PRELIMINARY; PRT; 15 AA.  
AC Q47832;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DB Beta-allophycocyanin (Fragment).  
OS Fremyella diplosiphon (Calothrix) PCC 7601.  
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyellales;  
NCBI\_TaxID=1197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=46233345; PubMed=3086870;  
RA Conley P.B.; Lemaux P.G.; Lomax T.L.; Grossman A.R.;  
RT "Genes encoding major light-harvesting polypeptides are clustered on  
the genome of the cyanobacterium Fremyella diplosiphon.";  
RT Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).  
DR EMBL; M13216; AAA24871.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 15 AA; 1644 MW; 97221656699F462F CRC64;

Query Match 41.3%; Score 19; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSFF 4  
Db 4 GSYF 7

---

RESULT 14  
ID Q53580 PRELIMINARY; PRT; 15 AA.  
AC Q53580;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Light-harvesting complex I alpha polypeptide (Fragment).  
GN PUF4.  
OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).  
OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1661;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92234963; PubMed=1569029;  
RA Richter P.; Brand M.; Drews G.;  
RA Characterization of LHI- and LHI+ Rhodobacter capsulatus pufA.

---

```

RT mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL; S97532; AAC6046.1; -
PT NON-TER 15 15
SQ SEQUENCE 15 AA; 2054 MW; 3561FE413591D31A CRC64;

Query Match 41.3%; Score 19; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 6.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFPSSELW 8
Db 2 SKFYKIV 8

RESULT 15
Q47893 PRELIMINARY; PRT; 15 AA.
ID Q47893;
AC Q47893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Beta-phycocyanin (Fragment).
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
OX NCBI_TaxID=1197;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3086870;
RX MEDLINE=86233345;
RA Conley B.B., Lemieux P.G., Lomax T.L., Grossman A.R. ;
RT "Genes encoding major light-harvesting polypeptides are clustered on
RT the genome of the cyanobacterium Fremyella diplosiphon." ;
RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).
DR EMBL; M13217; AAA24880.1; -
FT NON-TER 1 1
SQ SEQUENCE 15 AA; 1528 MW; 7FF2F65518F493D4 CRC64;

Query Match 41.3%; Score 19; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSFF 4
Db 4 GSYF 7

```

Search completed: September 20, 2004, 17:31:51  
Job time : 38 secs

Blank

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	BLOSUM62	HS11_DINPS	13	1	NP3_LYMST	P80180 lymnaea sta
2	19	Gapop 10.0 , Gapext 0.5	CA42_LITCHI	15	1	ALB2_TRASC	P81189 trachemys s
3	18	Searched: 141681 seqs, 52070155 residues	CXA2_CONGE	11	1	LPW_THETH	P05624 thermus the
4	18	Total number of hits satisfying chosen parameters:	KARA_BROPL	11	1	TKN4_SCYCHA	P41333 scyliorhinus ca
5	18	Minimum DB seq length: 11	UP01_CAEEL	15	1	FIBA_SYNCA	P14463 synceris ca
6	17	Maximum DB seq length: 15	UP01_CAEEL	11	1	MHB1_KLEPN	P80380 klebsiella
7	16	Post-processing: Minimum Match 0%	UP01_CAEEL	12	1	FAR7_PENMO	P83322 penaeus mon
8	16	Maximum Match 100%	UP01_CAEEL	12	1	UP01_CAEEL	P55054 caenorhabditis
9	16	Listing first 45 summaries	UP01_CAEEL	14	1	CXAI_CONCN	P56733 conus conso
10	16	Database : Swissprot_42:*	UP01_CAEEL	14	1	FIBA_HORSE	P14452 equus cabal
11	16	Scoring table: BLOSUM62	UP01_CAEEL	15	1	HS11_DINPS	P81083 pinus pinas
12	15	Gapop 10.0 . Gapext 0.5	UP01_CAEEL	11	1	CA42_LITCHI	P82992 litoria cit
13	15	Searched: 141681 seqs, 52070155 residues	UP01_CAEEL	13	1	CXA2_CONGE	P01520 conus geogr
14	15	Total number of hits satisfying chosen parameters:	UP01_CAEEL	14	1	KARA_BROPL	P2244 bromelia pl
15	14	Minimum DB seq length: 11	UP01_CAEEL	11	1	CORZ_PERAM	P11496 periplaneta
16	14	Maximum DB seq length: 15	UP01_CAEEL	12	1	HEP1_BACSE	P83054 bacteroides
17	14	Post-processing: Minimum Match 0%	UP01_CAEEL	13	1	CRTC_BOVIN	P28489 bos taurus
18	14	Maximum Match 100%	UP01_CAEEL	13	1	NP1_LYMST	P80178 lymnaea sta
19	14	Listing first 45 summaries	UP01_CAEEL	13	1	NP2_LYMST	P80179 lymnaea sta
20	14	Database : Swissprot_42:*	UP01_CAEEL	13	1	NP4_LYMST	P80181 lymnaea sta
21	14	Scoring table: BLOSUM62	UP01_CAEEL	13	1	NP5_LYMST	P80182 lymnaea sta
22	14	Gapop 10.0 , Gapext 0.5	UP01_CAEEL	13	1	TEJA_RANJA	P83307 rana japonica
23	14	Searched: 141681 seqs, 52070155 residues	UP01_CAEEL	14	1	DC34_MAIZE	P80640 sea molly (m)
24	14	Total number of hits satisfying chosen parameters:	UP01_CAEEL	14	1	ARCA_STRP5	P58827 streptococcus
25	14	Minimum DB seq length: 11	UP01_CAEEL	15	1	FKB7_PINPS	P81104 pinus pinas
26	14	Maximum DB seq length: 15	UP01_CAEEL	15	1	MM01_RAT	P81563 ratmus norvegicus
27	14	Post-processing: Minimum Match 0%	UP01_CAEEL	15	1	RBS_PHYPA	P80657 physcomitrium
28	14	Maximum Match 100%	UP01_CAEEL	15	1	UC16_MAIZE	P80622 zea mays (m)
29	13	Database : Swissprot_42:*	UP01_CAEEL	15	1	NUHM_CANFA	P49820 canis familiaris
30	13	Scoring table: BLOSUM62	UP01_CAEEL	13	1	UR2_POLSP	P81022 polyodon sp
31	13	Gapop 10.0 , Gapext 0.5	UP01_CAEEL	13	1	ADFB_TENM0	P83109 tenebrio molitor
32	13	Total number of hits satisfying chosen parameters:	UP01_CAEEL	13	1	ORCK_ORCL1	P37086 orconectes
33	13	Minimum DB seq length: 11	UP01_CAEEL	13	1	UN02_PINPS	P81667 pinus pinas

ALIGNMENTS							
RESULT 1							
NP3_LYMST							
ID	NP3_LYMST	STANDARD;	PRT;	13 AA.			
AC	P80180;						
DT	01-JUL-1993	(Rel. 26, Created)					
DT	01-JUL-1993	(Rel. 26, Last sequence update)					
DT	01-JUL-1993	(Rel. 26, Last annotation update)					
DE	Lymnaea-de-amide 3.						
OS	Lymnaea stagnalis (Great pond snail).						
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora; Lymnaeoidea; Lymnaeidae; Lymnaea.						
OX	NCBI_TaxID=6523;						
[1]	RN						
RP	SEQUENCE.						
RC	TISSUE;Ganglion;						
RX	PubMed=93239777;						
RA	Johnsen A.H.; Rehfeld J.F.;						
RT	"Lymnaeidae", a new family of neuropeptides from the pond snail.						
RT	Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in invertebrates?;						
RT	Eur. J. Biochem. 213:875-879(1993).						
CC	-1. SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.						
DR	CCP1; S32473; S32473.						
KW	Neuropeptide; Amidation.						
FT	MOD_RES	13	13				
FT	UNSDRE	12	12				
FT	SEQUENCE	13 AA;	1462	MW:	9CA07BA3F5D5B865	CRC64;	
Query	Match	43.5%;	Score 20;	DB 1;	Length 13;		
Best	Local Similarity	66.7%;	Pred. No. 5.e+02;				
Matches	4;	Conservative	1;	Mismatches	1;	Indels	0;
QY	1 GSFFSE 6						
Db	7 GSAFSD 12						
RESULT 2							
ID	ALB2_TRASC	STANDARD;	PRT;	15 AA.			
AC	P81189;						
DT	15-JUL-1998	(Rel. 36, Created)					
DT	15-JUL-1998	(Rel. 36, Last sequence update)					
DT	15-PBB-2003	(Rel. 41, Last annotation update)					
DE	68 kDa serum albumin (Alb-2) (Fragment).						
OS	Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;						
OT	Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemyidae.						
NCBI_TaxID=34903;	[1]						
RN	SEQUENCE.						
RX	PubMed=9440230;						
RA	Brown M.A.; Chambers G.K., Licht P.;						
RT	Purification and partial amino acid sequences of two distinct						
RT	proteins from turtle plasma;"						
RL	Comp. Biochem. Physiol. 118B:367-374 (1997).						

CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K+, fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Plasma.

CC -!- MISCELLANEOUS: In the red-eared slider turtle, there are two forms of albumin, ALB-1 and ALB-2.

CC -!- SIMILARITY: Belongs to the ALB/AFP/VDB family.

DR InterPro: IPR000264; Serum\_albumin.

PROSITE: PS00212; ALBUMIN; PARTIAL.

KW Metal-binding; Lipid-binding.

FT NON\_TER 15 15 SEQUENCE 15 AA; 1733 MW; 4B7422B89FF73223 CRC64;

Query Match Score 19; DB 1; Length 15;  
Best Local Similarity 57.1%; Pred. No. 9.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GSFFSEED 7  
Db 9 GHXFXEL 15

---

RESULT 3

LPW THETH THETH STANDARD; PRT; 11 AA.

ID LPW THETH THETH STANDARD; PRT; 11 AA.

AC P0564;

DT 01-NOV-1988 (Rel. 09, Created)

RT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DB Trp operon leader peptide.

GN TRPL.

CQ Thermus thermophilus.

CC Bacterium; Deinococcus-Thermus; Deinococci; Thermales; Thermacaea;

OX NCBI\_TAXID=274.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HBB / ATCC 27634;

RC MEDLINE=89000781; PubMed=2844259;

RA Sato S., Nakada Y., Kanaya S., Tanaka T.;

RT "Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and trpG."

RL Biophys. Acta 950:303-312 (1988).

CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS OF TRYPTOPHAN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; X0744; CAA30565.1; -.

KW TRYPTOPHAN biosynthesis; Leader peptide.

SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match Score 18; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SELW 8  
Db 5 SALW 8

---

RESULT 4

TkNA SCYCA STANDARD; PRT; 11 AA.

ID TkNA\_SCYCA STANDARD; PRT; 11 AA.

AC P41333;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB Substance\_P.

OS Scylloarinus canicula (Spotted catshark)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichtyes;

OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;

OC Scylloarinidae; Scyliorhinus.

NCBI\_TAXID=7830;

RN [1]

RP SEQUENCE.

RC TISSUE\_Brain;

RX MEDLINE=93292508; PubMed=7685693;

RA Waugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;

RT "Primary structures and biological activities of substance P-related peptides from the brain of the dogfish, *Scyliorhinus canicula*."

RL Eur. J. Biochem. 214:469-474 (1993).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretegogues, and contract (directly or indirectly) many smooth muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PTR; S33300; S33300.

DR InterPro; IPR02040; Tachy\_Neurokinin.

DR PROSITE; PS00267; TACHYKININ\_1.

KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.

FT MODES 11 11 AMINATION.

SEQUENCE 11 AA; 1278 MW; 214860DEC9D6DB67 CRC64;

Query Match Score 18; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSFF 4  
Db 5 GQFF 8

---

RESULT 5

FIBA\_SYNCA STANDARD; PRT; 15 AA.

ID FIBA\_SYNCA STANDARD; PRT; 15 AA.

AC P14463;

DT 01-JAN-1990 (Rel. 13, Created)

RT 01-JAN-1990 (Rel. 13, Last sequence update)

DB DE 10-OCT-2003 (Rel. 42, Last annotation update)

GN Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).

FGA.

OS Syncerous caffer (Cape buffalo).

OC Bucaryota; Metazoa; Chordata; Craniata; Vertebrata; Peccora; Bovoidea;

CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccora; Bovoidea;

CC Bovidae; Bovinae; Syncerus.

NCBI\_TAXID=9970;

RN [1]

RP SEQUENCE.

RC MEDLINE=67209145; PubMed=6032721;

RA Doobie R.F., Schubert D., Schwartz S.A.;

RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I. Dromedary camel, mule deer, and cape buffalo."

RL Arch. Biochem. Biophys. 118:456-467 (1967).

CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.

CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.

KW Blood coagulation; Plasma.

FT PEPTIDE 1 15 FIBRINOPEPTIDE A.

FT NON\_TER 15 15 SQ SEQUENCE 15 AA; 1480 MW; 4E998EA5FQB41CC6 CRC64;

Query Match Similarity 39.1%; Score 18; DB 1; Length 15;	Best Local Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	FT SQ	MOD RES SEQUENCE	12 AA;	12 MW;	AMIDATION.
		Query Match	Score 16;	DB 1;	Length 12;	
		Best Local Matches 3; Conservative 0;	Score 16;	Pred. No. 2.9e+03;	Pred. No. 2.9e+03;	
Qy 1 GSFFSE 6	Dy 5 GBFLAE 10	Qy	0; Mismatches 1;	0; Indels 0;	0; Gaps 0;	
		Qy	1 GSFF 4	Db	9 GSIF 12	
<b>RESULT 6</b>						
MHBI KLEPN	STANDARD;	PRT;	11 AA.			
ID MHBI KLEPN						
AC P80580;						
DT 01-OCT-1996 (Rel. 34, Created)						
DT 01-OCT-1996 (Rel. 34, Last sequence update)						
DT 01-NOV-1997 (Rel. 35, Last annotation update)						
DB Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).						
GN MHBI.						
OS Klebsiella pneumoniae.						
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;						
OC Enterobacteriaceae; Klebsiella.						
NCBI_TAXID=573;						
RN [1]						
RP SEQUENCE.						
RX MEDLINE=96349117; PubMed=8760924;						
RA Robson N.D., Parrott S., Cooper R.A.						
RT "In vitro formation of a catabolic plasmid carrying Klebsiella pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-hydroxybenzoate."						
RT Microbiology 142:2115-2120(1996).						
CC 1-CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.						
KW Isomerase.						
FT NON TER 11 AA; 11 MW;	11E0E2DD49C9D5AB CRC64;					
SQ SEQUENCE 11 AA;	1387 MW;					
<b>RESULT 7</b>						
FAR7_PENMO	STANDARD;	PRT;	12 AA.			
ID FAR7_PENMO						
AC P83322;						
DT 28-FEB-2003 (Rel. 41, Created)						
DT 28-FEB-2003 (Rel. 41, Last sequence update)						
DT 28-FEB-2003 (Rel. 41, Last annotation update)						
DE FMRFamide-like neuropeptide FLP7 (GYRKPFPNSIF-amide).						
OS Penaeus monodon (Penaeo shrimp).						
EU Eukaryota; Arthropoda; Crustacea; Malacostraca;						
OC Eumalacostraca; Decapoda; Dendrobranchiata; Penaeoidea;						
OC Penaeidae; Penaeus.						
NCBI_TAXID=6687;						
RN [1]						
RP SEQUENCE, AND MASS SPECTROMETRY.						
RC TISSUE=Eye stalk;						
RC MEDLINE=21956277; PubMed=11159015;						
RA Sithigorngul P., Puwan J., Krungrasen C., Longrunt S., Chaivisuthangkura P., Sithigorngul W., Petson A.;						
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk of the giant tiger prawn Penaeus monodon."						
RT Comp. Biochem. Physiol. 131B:325-337 (2002).						
CC -1- SUBCELLULAR LOCATION: Secreted.						
CC -1- MASS SPECTROMETRY: MW=138.4; METHOD=MALDI.						
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.						
CC GO: GO:0007218; P:Neuropeptide signaling pathway; TAS.						
KW Neuropeptide; Amidation.						

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 family.  
 CC PIR: A58963; A58963;  
 DR PDB: 1B45; 09-JUL-95.  
 KW Post-synaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
 FT PEPTIDE 1 14 ALPHA-CONOTOXIN CNIA.  
 FT PEPTIDE 3 14 ALPHA-CONOTOXIN CNIB.  
 FT DISULFID 3 8  
 FT DISULFID 4 14 AMIDATION.  
 FT MOD RES 14 14  
 FT HELIX 6 8  
 FT TURN 9 10  
 SQ SEQUENCE 14 AA; 1548 MW; D8EE9196BF5E5BD CRC64;  
 Query Match 34.8%; Score 16; DB 1; Length 14;  
 Best Local Similarity 40.0%; Pred. No. 3.3e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSFFS 5  
 | :|  
 Db 9 GKYY 13

RESULT 10  
 FIBA\_HORSE STANDARD PRT; 14 AA.  
 ID FIBA\_HORSE  
 AC P14452;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 10-JAN-2003 (Rel. 42, Last sequence update)  
 DE Fibrinogen alpha chain [Contains: Fibronopeptide A] (Fragment).  
 GN EQUUS CABALLUS (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 NCBI\_TaxID=9736;  
 RN SEQUENCE.  
 RA Blomback B., Blomback M., Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals.";  
 RL Acta Chem. Scand. 19:1789-1794(1965).  
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.  
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.  
 KW Blood coagulation; Plasma.  
 FT PEPTIDE 1 14 FIBRINOPEPTIDE A.  
 SQ SEQUENCE 14 AA; 1517 MW; 4E99EB63C2A15E7 CRC64;  
 Query Match 34.8%; Score 16; DB 1; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Gaps 0;  
 QY 1 GSFFS 6  
 | :|  
 Db 4 GEFLME 9

RESULT 12  
 CA42\_LITCI STANDARD; PRT; 11 AA.  
 ID CA42\_LITCI  
 AC P82052;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Caerulein 4.2/4.2/4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC PeLodryadinae; Litoria.  
 NCBI\_TaxID=94170;  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RP TISSUE=Skin secretion;  
 RX MEDLINE=2005701; PubMed=10589099;  
 RA Walnitz P.A.; Bowie J.H.; Tyler M.J.;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

mountains tree frog *Litoria citropa*. Part 1. Sequence determination using electrospray mass spectrometry.";

Rapid Commun. Mass Spectrom. 13:2498-2502 (1999).

-!- FUNCTION: Hypotensive neuropeptide (Probable).

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE/SPECIFICITY: Skin dorsal glands.

-!- PTM: Isoform 4.2X4 differs from isoform 4.2 in not being sulfated.

CC -!- MASS SPECTROMETRY; MW=1404; METHOD=Electrospray.

CC !- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; FALSE NEG.

KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;

KW Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 4 4 SULFATION.

FT MOD RES 11 11 AMIDATION.

SEQUENCE 11 AA; 1344 MW; 10DABB94F5BB861BB CRC64;

Query Match Score 32.6%; Score 15; DB 1; Length 11;

Best Local Similarity 75.0%; Pred. No. 4e+03; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSFF 4

Db 6 GSHF 9

RESULT 13

ID CXA2\_CONGE ID KARA\_BROPL STANDARD; PRT; 13 AA.

AC P01520; AC ID KARA\_BROPL STANDARD; PRT; 13 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-conotoxin GI.

OS Conus geographus (Geography cone).

OC Bivalvia; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

NCBI\_TaxID=6491; [1]

RP SEQUENCE.

RX MEDLINE=81191854; PubMed=7014556;

RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.; RT "Peptide toxins from *Conus geographus* venom.";

RL J. Biol. Chem. 256:4734-4740(1981). [2]

RP DISULFIDE BONDS.

RX MEDLINE=84280842; PubMed=6466616;

RA Gray W.R., Luque F.A., Galve R., Atherton E., Sheppard R.C., Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M., Cruz L.J., Rivier J.; RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of iodinated derivatives.";

RT Biochemistry 23:2796-2802(1984).

CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE/SPECIFICITY: Expressed by the venom duct.

CC -!- SIMILARITY: Belongs to the conotoxin A superfamily. Alpha-type family.

DR PIR; A01183; NTXN2G.

DR HSSP; PS5973; 1B45.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;

KW Acetylcholine receptor inhibitor; Amidation.

FT DISULFID 2 7

FT DISULFID 3 13 AMIDATION.

FT MOD RES 13 13 AMIDATION.

SEQUENCE 13 AA; 1422 MW; DEEE831C39297EBD CRC64;

Query Match Score 32.6%; Score 15; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. No. 4.8e+03; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFS 5

Db 8 GKHF 12

RESULT 14

KARA\_BROPL ID KARA\_BROPL STANDARD; PRT; 14 AA.

AC P2247;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Karatasin (EC 3.4.22.-) (Fragment).

OS Bromelia plumieri (Karatas).

OC Spermatophytida; Magnoliophyta; Streptophyta; Embryophyta; Tracheophyta;

OC Bivalvia; Viridiplantae; Magnoliopsida; Liliopsida; Poales; Bromeliaceae;

OC Bromelia.

NCBI\_TaxID=4617; [1]

RX RN

RP SEQUENCE.

MEDLINE=90344224; PubMed=1368518;

RA Montes C., Amador M., Cuevas D., Cordoba F.; RT "Subunit structure of karatasin, the proteinase isolated from Bromelia plumieri (karatas)." Agric. Biol. Chem. 54:17-24 (1990).

RL DR InterPro; IPR000169; SHPr0t\_acsite.

CC -!- SIMILARITY: Dimer of two small subunits linked by disulfide bonds.

CC DR PROSITE; PS00139; THIOL\_PROTEASE\_CYS; PARTIAL.

CC DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; PARTIAL.

CC DR PROSITE; PS00640; THIOL\_PROTEASE ASN; PARTIAL.

CC KW Hydrolase; Thio protease.

FT NON\_TER 14 14 SEQNECE 14 AA; 1602 MW; FDA156893F0834FA CRC64;

Query Match Score 32.6%; Score 15; DB 1; Length 14;

Best Local Similarity 66.7%; Pred. No. 5.2e+03; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ELW 8

Db 3 ETW 5

RESULT 15

CORZ\_2F6AM ID CORZ\_2F6AM STANDARD; PRT; 11 AA.

AC P1496;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Corazonin.

OS Periplaneta americana (American cockroach).

OC Burkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.

NCBI\_TaxID=6978; [1]

RN RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=9323572; PubMed=2753132;

RA Veenstra J.A.; RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach,"

RL FEBS Lett. 250:231-234 (1989).

CC -!- FUNCTION: Cardioactive Peptide. Corazonin is probably involved in the physiological regulation of the heart beat.

CC -!- SUBCELLULAR LOCATION: Secreted.

DR PIR; S05002; S05002.

KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
MOD RES 1  
FT PYRROLIDONE CARBOXYLIC ACID.  
MOD\_PBS 11  
FT AMIDATION.  
SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;  
Query Match 30.4%; Score 14; DB 1; Length 11;  
Best Local Similarity 40.0%; Pred. No. 6.3e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 FSELW 8  
: 5 YSRGW 9  
Db

Search completed: September 20, 2004, 17:31:08  
Job time : 10 secs

Page 1

Copyright	GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.	run on:	September 20, 2004, 17:29:05 ; Search time 15 Seconds (without alignments)	total number of hits satisfying chosen parameters:	1421																																																																																																																																																																																																																																																																																																									
MM protein - protein search, using sw model	AUDET-SRQ1 perfect score: 46 sequence: 1 gsfsefw 8	scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	searched:	28336 seqs, 96191526 residues																																																																																																																																																																																																																																																																																																									
					total minimum DB seq length: 11 maximum DB seq length: 15																																																																																																																																																																																																																																																																																																									
					post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries																																																																																																																																																																																																																																																																																																									
					database : PTR 78: 1: Pir1: 2: Pir2: 3: Pir3: 4: Pir4: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.																																																																																																																																																																																																																																																																																																									
					SUMMARIES																																																																																																																																																																																																																																																																																																									
					<table border="1"> <thead> <tr> <th>result</th> <th>No.</th> <th>Score</th> <th>Query</th> <th>Match</th> <th>Length</th> <th>DB</th> <th>ID</th> <th>Description</th> </tr> </thead> <tbody> <tr> <td>1</td> <td>23</td> <td>50.0</td> <td></td> <td>15</td> <td>2</td> <td>PHI1613</td> <td></td> <td>Ig H chain V-D-J r</td> </tr> <tr> <td>2</td> <td>22</td> <td>47.8</td> <td></td> <td>15</td> <td>2</td> <td>F29501</td> <td></td> <td>fibrinopeptide A -</td> </tr> <tr> <td>3</td> <td>20</td> <td>43.5</td> <td></td> <td>13</td> <td>2</td> <td>S32473</td> <td></td> <td>lymnaDFamide 3 -</td> </tr> <tr> <td>4</td> <td>20</td> <td>43.5</td> <td></td> <td>13</td> <td>2</td> <td>H56046</td> <td></td> <td>urinary tract ston</td> </tr> <tr> <td>5</td> <td>19</td> <td>41.3</td> <td></td> <td>15</td> <td>2</td> <td>I29501</td> <td></td> <td>fibrinopeptide A -</td> </tr> <tr> <td>6</td> <td>19</td> <td>41.3</td> <td></td> <td>15</td> <td>2</td> <td>S43956</td> <td></td> <td>Ig mu chain V regi</td> </tr> <tr> <td>7</td> <td>18</td> <td>39.1</td> <td>LFTWWB</td> <td>11</td> <td>2</td> <td>S33300</td> <td></td> <td>probable trpBG lea</td> </tr> <tr> <td>8</td> <td>18</td> <td>39.1</td> <td></td> <td>11</td> <td>2</td> <td>A17150</td> <td></td> <td>probable substance</td> </tr> <tr> <td>9</td> <td>18</td> <td>39.1</td> <td></td> <td>14</td> <td>2</td> <td>PH1172</td> <td></td> <td>glucose 1-dehydrog</td> </tr> <tr> <td>10</td> <td>18</td> <td>39.1</td> <td></td> <td>15</td> <td>2</td> <td>PH1366</td> <td></td> <td>Ig heavy chain DJ</td> </tr> <tr> <td>11</td> <td>17</td> <td>37.0</td> <td></td> <td>12</td> <td>2</td> <td>PH1189</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>12</td> <td>17</td> <td>37.0</td> <td></td> <td>12</td> <td>2</td> <td>PH1180</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>13</td> <td>17</td> <td>37.0</td> <td></td> <td>12</td> <td>2</td> <td>PH1183</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>14</td> <td>17</td> <td>37.0</td> <td></td> <td>12</td> <td>2</td> <td>PH1188</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>15</td> <td>17</td> <td>37.0</td> <td></td> <td>12</td> <td>2</td> <td>PH1172</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>16</td> <td>17</td> <td>37.0</td> <td></td> <td>12</td> <td>2</td> <td>PH1175</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>17</td> <td>17</td> <td>37.0</td> <td></td> <td>14</td> <td>2</td> <td>B44854</td> <td></td> <td>L-2,4-diaminobuty</td> </tr> <tr> <td>18</td> <td>17</td> <td>37.0</td> <td></td> <td>14</td> <td>2</td> <td>PH1448</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>19</td> <td>17</td> <td>37.0</td> <td></td> <td>12</td> <td>2</td> <td>PH1450</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>20</td> <td>17</td> <td>37.0</td> <td></td> <td>14</td> <td>2</td> <td>PH0945</td> <td></td> <td>T-cell receptor be</td> </tr> <tr> <td>21</td> <td>17</td> <td>37.0</td> <td></td> <td>15</td> <td>2</td> <td>S26516</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>22</td> <td>17</td> <td>37.0</td> <td></td> <td>15</td> <td>2</td> <td>S26524</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>23</td> <td>17</td> <td>37.0</td> <td></td> <td>15</td> <td>2</td> <td>S26527</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>24</td> <td>17</td> <td>37.0</td> <td></td> <td>15</td> <td>2</td> <td>S26528</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>25</td> <td>17</td> <td>37.0</td> <td></td> <td>15</td> <td>2</td> <td>S26534</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>26</td> <td>17</td> <td>37.0</td> <td></td> <td>15</td> <td>2</td> <td>PH1436</td> <td></td> <td>T-cell receptor al</td> </tr> <tr> <td>27</td> <td>16.5</td> <td>35.9</td> <td></td> <td>15</td> <td>2</td> <td>PH1365</td> <td></td> <td>Ig heavy chain DJ</td> </tr> <tr> <td>28</td> <td>16</td> <td>34.8</td> <td></td> <td>11</td> <td>2</td> <td>C53652</td> <td></td> <td>rhr protein -</td> </tr> <tr> <td>29</td> <td>16</td> <td>34.8</td> <td></td> <td>11</td> <td>2</td> <td>PTC302</td> <td></td> <td>gene HEXA protein</td> </tr> <tr> <td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td> <td>lysmaDFamide 3 - great pond snail</td> </tr> <tr> <td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td> <td>lysmaDFamide 3 - Ig heavy chain CRD</td> </tr> <tr> <td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td> <td>lysmaDFamide 3 - Ig heavy chain CRD</td> </tr> </tbody> </table>	result	No.	Score	Query	Match	Length	DB	ID	Description	1	23	50.0		15	2	PHI1613		Ig H chain V-D-J r	2	22	47.8		15	2	F29501		fibrinopeptide A -	3	20	43.5		13	2	S32473		lymnaDFamide 3 -	4	20	43.5		13	2	H56046		urinary tract ston	5	19	41.3		15	2	I29501		fibrinopeptide A -	6	19	41.3		15	2	S43956		Ig mu chain V regi	7	18	39.1	LFTWWB	11	2	S33300		probable trpBG lea	8	18	39.1		11	2	A17150		probable substance	9	18	39.1		14	2	PH1172		glucose 1-dehydrog	10	18	39.1		15	2	PH1366		Ig heavy chain DJ	11	17	37.0		12	2	PH1189		T-cell receptor al	12	17	37.0		12	2	PH1180		T-cell receptor al	13	17	37.0		12	2	PH1183		T-cell receptor al	14	17	37.0		12	2	PH1188		T-cell receptor al	15	17	37.0		12	2	PH1172		T-cell receptor al	16	17	37.0		12	2	PH1175		T-cell receptor al	17	17	37.0		14	2	B44854		L-2,4-diaminobuty	18	17	37.0		14	2	PH1448		T-cell receptor al	19	17	37.0		12	2	PH1450		T-cell receptor al	20	17	37.0		14	2	PH0945		T-cell receptor be	21	17	37.0		15	2	S26516		T-cell receptor al	22	17	37.0		15	2	S26524		T-cell receptor al	23	17	37.0		15	2	S26527		T-cell receptor al	24	17	37.0		15	2	S26528		T-cell receptor al	25	17	37.0		15	2	S26534		T-cell receptor al	26	17	37.0		15	2	PH1436		T-cell receptor al	27	16.5	35.9		15	2	PH1365		Ig heavy chain DJ	28	16	34.8		11	2	C53652		rhr protein -	29	16	34.8		11	2	PTC302		gene HEXA protein									lysmaDFamide 3 - great pond snail									lysmaDFamide 3 - Ig heavy chain CRD									lysmaDFamide 3 - Ig heavy chain CRD
result	No.	Score	Query	Match	Length	DB	ID	Description																																																																																																																																																																																																																																																																																																						
1	23	50.0		15	2	PHI1613		Ig H chain V-D-J r																																																																																																																																																																																																																																																																																																						
2	22	47.8		15	2	F29501		fibrinopeptide A -																																																																																																																																																																																																																																																																																																						
3	20	43.5		13	2	S32473		lymnaDFamide 3 -																																																																																																																																																																																																																																																																																																						
4	20	43.5		13	2	H56046		urinary tract ston																																																																																																																																																																																																																																																																																																						
5	19	41.3		15	2	I29501		fibrinopeptide A -																																																																																																																																																																																																																																																																																																						
6	19	41.3		15	2	S43956		Ig mu chain V regi																																																																																																																																																																																																																																																																																																						
7	18	39.1	LFTWWB	11	2	S33300		probable trpBG lea																																																																																																																																																																																																																																																																																																						
8	18	39.1		11	2	A17150		probable substance																																																																																																																																																																																																																																																																																																						
9	18	39.1		14	2	PH1172		glucose 1-dehydrog																																																																																																																																																																																																																																																																																																						
10	18	39.1		15	2	PH1366		Ig heavy chain DJ																																																																																																																																																																																																																																																																																																						
11	17	37.0		12	2	PH1189		T-cell receptor al																																																																																																																																																																																																																																																																																																						
12	17	37.0		12	2	PH1180		T-cell receptor al																																																																																																																																																																																																																																																																																																						
13	17	37.0		12	2	PH1183		T-cell receptor al																																																																																																																																																																																																																																																																																																						
14	17	37.0		12	2	PH1188		T-cell receptor al																																																																																																																																																																																																																																																																																																						
15	17	37.0		12	2	PH1172		T-cell receptor al																																																																																																																																																																																																																																																																																																						
16	17	37.0		12	2	PH1175		T-cell receptor al																																																																																																																																																																																																																																																																																																						
17	17	37.0		14	2	B44854		L-2,4-diaminobuty																																																																																																																																																																																																																																																																																																						
18	17	37.0		14	2	PH1448		T-cell receptor al																																																																																																																																																																																																																																																																																																						
19	17	37.0		12	2	PH1450		T-cell receptor al																																																																																																																																																																																																																																																																																																						
20	17	37.0		14	2	PH0945		T-cell receptor be																																																																																																																																																																																																																																																																																																						
21	17	37.0		15	2	S26516		T-cell receptor al																																																																																																																																																																																																																																																																																																						
22	17	37.0		15	2	S26524		T-cell receptor al																																																																																																																																																																																																																																																																																																						
23	17	37.0		15	2	S26527		T-cell receptor al																																																																																																																																																																																																																																																																																																						
24	17	37.0		15	2	S26528		T-cell receptor al																																																																																																																																																																																																																																																																																																						
25	17	37.0		15	2	S26534		T-cell receptor al																																																																																																																																																																																																																																																																																																						
26	17	37.0		15	2	PH1436		T-cell receptor al																																																																																																																																																																																																																																																																																																						
27	16.5	35.9		15	2	PH1365		Ig heavy chain DJ																																																																																																																																																																																																																																																																																																						
28	16	34.8		11	2	C53652		rhr protein -																																																																																																																																																																																																																																																																																																						
29	16	34.8		11	2	PTC302		gene HEXA protein																																																																																																																																																																																																																																																																																																						
								lysmaDFamide 3 - great pond snail																																																																																																																																																																																																																																																																																																						
								lysmaDFamide 3 - Ig heavy chain CRD																																																																																																																																																																																																																																																																																																						
								lysmaDFamide 3 - Ig heavy chain CRD																																																																																																																																																																																																																																																																																																						
					RESULTS																																																																																																																																																																																																																																																																																																									
					1	Qy	3 FFSEIW 8	Score 22; DB 2; Length 15;																																																																																																																																																																																																																																																																																																						
					Db		9 YFTMLW 14	Pred. No. 3.2e+02; Mismatches 2; Conservative 1; Indels 0; Gaps 0																																																																																																																																																																																																																																																																																																						
					RESULT 1	Query Match 50.0%; Best Local Similarity 50.0%; Matches 3;保守性 3; Mismatches 2; Indels 1; Gaps 0																																																																																																																																																																																																																																																																																																								
					PHI1613	Ig H chain V-D-J region (clone B-Less 17) - mouse (fragment)																																																																																																																																																																																																																																																																																																								
					C;Species: Mus musculus (house mouse)																																																																																																																																																																																																																																																																																																									
					C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999																																																																																																																																																																																																																																																																																																									
					C;Accession: PHI1613																																																																																																																																																																																																																																																																																																									
					R;Levinson, D.A.; Campos-Torres, J.; Leder, P.																																																																																																																																																																																																																																																																																																									
					J. Exp. Med. 178, 317-329, 1993																																																																																																																																																																																																																																																																																																									
					A;Title: Molecular characterization of transgene-induced immunodeficiency in B-lymphocytes																																																																																																																																																																																																																																																																																																									
					A;Reference number: PH1580; PMID:93301609; PMID:8315387																																																																																																																																																																																																																																																																																																									
					A;Accession: PHI1613																																																																																																																																																																																																																																																																																																									
					A;Molecule type: DNA																																																																																																																																																																																																																																																																																																									
					A;Residues: 1-15 <LEV>																																																																																																																																																																																																																																																																																																									
					C;Experimental source: bone marrow pre-B lymphocyte																																																																																																																																																																																																																																																																																																									
					C;Keywords: Immunoglobulin																																																																																																																																																																																																																																																																																																									
					C;Key words: Immunoglobulin																																																																																																																																																																																																																																																																																																									
					RESULT 2	Query Match 50.0%; Best Local Similarity 50.0%; Matches 3;保守性 3; Mismatches 2; Indels 1; Gaps 0																																																																																																																																																																																																																																																																																																								
					F29501	fibrinopeptide A - wombat																																																																																																																																																																																																																																																																																																								
					C;Species: Vombatidae gen. sp. (wombat)																																																																																																																																																																																																																																																																																																									
					C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000																																																																																																																																																																																																																																																																																																									
					C;Accession: F29501																																																																																																																																																																																																																																																																																																									
					R;Blomhaeck, B.; Blomhaeck, M.; Hann, C.																																																																																																																																																																																																																																																																																																									
					unpublished results, cited by Blomhaeck, B., and Blomhaeck, M., in Chemosphere																																																																																																																																																																																																																																																																																																									
					A;Reference number: A29501																																																																																																																																																																																																																																																																																																									
					A;Accession: F29501																																																																																																																																																																																																																																																																																																									
					A;Status: Preliminary																																																																																																																																																																																																																																																																																																									
					A;Molecule type: protein																																																																																																																																																																																																																																																																																																									
					A;Residues: 1-15 <BIO>																																																																																																																																																																																																																																																																																																									
					C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology																																																																																																																																																																																																																																																																																																									
					Query Match 47.8%; Best Local Similarity 66.7%; Matches 4;保守性 4; Mismatches 1; Indels 1; Gaps 0																																																																																																																																																																																																																																																																																																									
					Qy	1 GSFPSE 6																																																																																																																																																																																																																																																																																																								
					Db	:    5 GSFLAE 10																																																																																																																																																																																																																																																																																																								

C;Species: *Lymnaea stagnalis* (great pond snail)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C;Accession: S32473  
R;Johnsen, A.H.; Rehfeld, J.F.  
Bur. J. Biochem. 213, 875-879, 1993  
A;Title: Lymnaeidae, a new family of neuropeptides from the pond snail, *Lymnaea stagnalis*  
A;Reference number: S32471; MUID:93238777; PMID:8477756  
A;Accession: S32473  
A;Molecule type: protein  
A;Residues: 1-13 <D0H>  
A;Cross-references: PIDN:AAB26364\_1; PID:9299831  
A;Experimental source: ganglia  
C;Keywords: amidated carboxyl end; neuropeptide F;13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match	43.5%;	Score 20;	DB 2;	Length 13;			
Best Local Similarity	66.7%;	Pred. No.	1.1e+03;				
Matches	4;	Conservative	1;	Mismatches	1;	Indels	0;
Qy	1 GSFFSE 6						
Db	7 GSAFSD 12						

RESULT 4  
H56046  
urinary tract stone matrix protein 10, 42K - human (fragment)  
C;Species: *Homo sapiens* (man)  
C;Accession: HS6046  
R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.  
Submitted to the Protein Sequence Database, February 1995  
A;Description: Isolation, characterization and sequence of stone proteins.  
A;Reference number: A56046  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <B1N>

Query Match	43.5%;	Score 20;	DB 2;	Length 13;			
Best Local Similarity	50.0%;	Pred. No.	1.1e+03;				
Matches	3;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	2 SEFSEL 7						
Db	3 SYFNDL 8						

RESULT 5  
I29501  
fibrinopeptide A - kangaroo  
C;Species: *Macropus* sp. (kangaroo)  
C;Accession: I29501  
R;Blomhaeck, B.; Blomhaeck, M.; Hann, C.  
unpublished results, cited by Blomhaeck, B., and Blomhaeck, M., in Chemotaxonomy and Serology  
A;Reference number: A29501  
A;Accession: I29501  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <B1O>  
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match	41.3%;	Score 19;	DB 2;	Length 15;			
Best Local Similarity	50.0%;	Pred. No.	1.9e+03;				
Matches	3;	Conservative	2;	Mismatches	1;	Indels	0;
Qy	1 GSFFSE 6						
Db	5 GTFLAE 10						

RESULT 6

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 GSFFSEL 7 Db 6 GGFA~~S~~AL 12

RESULT 9  
 A17150 glucose 1-dehydrogenase (NAD) (EC 1.1.1.118) - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 03-Jun-2002  
 C;Accession: A17150  
 R;Franzen, B.; Carrubba, C.; Feingold, D.S.; Ashcom, J.; Franzen, J.S.  
 A;Title: Amino acid sequence of the tryptic peptide containing the catalytic-site thiol  
 A;Reference number: A17150; MUID:82182061; PMID:6896145  
 A;Molecule type: protein  
 A;Residues: 1-14 <WAS>  
 C;Keywords: NAD; oxidoreductase

Query Match 39.1%; Score 18; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 2.e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GSFFSEL 6  
 Db 7 GSCFZZ 12

RESULT 10  
 PH1366 Ig heavy chain DJ region (clone C111-106) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1366  
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A;Reference number: PH1302; MUID:93034761; PMID:1460419  
 A;Molecule type: DNA  
 A;Residues: 1-15 <WAS>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 39.1%; Score 18; DB 2; Length 15;  
 Best Local Similarity 16.7%; Pred. No. 3.e+03;  
 Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 3 FFSELW 8  
 Db 6 YYGDYW 11

RESULT 11  
 PH1189 T-cell receptor alpha chain V region (Cw3/2c3) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C;Accession: PH1189  
 R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992  
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A;Reference number: S26512; MUID:92364546; PMID:1380061  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 3.7.e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 12  
 PH1180 T-cell receptor alpha chain V region (Cw3/5B8) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C;Accession: PH1180  
 R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992  
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A;Reference number: S26512; MUID:92364546; PMID:1380061  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 3.7.e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 13  
 PH1183 T-cell receptor alpha chain V region (Cw3/A8) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C;Accession: PH1183  
 R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992  
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A;Reference number: S26512; MUID:92364546; PMID:1380061  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 3.7.e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 14  
 PH1188 T-cell receptor alpha chain V region (Cw3/Cas11) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C;Accession: PH1188  
 R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992  
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A;Reference number: S26512; MUID:92364546; PMID:1380061  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 3.7.e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GSFFSPL 7  
       | | |  
       6 GGRASAL 12

---

RESULT 15  
 PH1172 T-cell receptor alpha chain V region (Cw3/Cas15) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C;Accession: PH1172  
 R;Catanova, J.I.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992.  
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A;Reference number: S26512; PMID:92364546; PMID:1380061  
 A;Accession: PH1172  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <CAS>  
 Query Match 37.0%; Score 17; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 3.7e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GSFFSPL 7  
       | | |  
       6 GGRASAL 12

Search completed: September 20, 2004, 17:32:10  
 Job time : 16 secs





PF 21-SEP-1999; 99DE-01045211.  
 XX  
 PR 21-SEP-1999; 99DE-01045211.  
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;  
 PI DR WPI: 2001-301259/32.  
 XX New autoantibody-binding peptides with an amino acid sequence  
 PT corresponding a beta-1-adrenergic receptor group useful for treating  
 PT dilatative cardiomyopathy.  
 XX PS: Claim 2; Page 5; 8pp; German.

XX This invention describes novel peptides (I) with an amino acid sequence  
 CC corresponding a beta-1-adrenergic receptor group recognized by  
 CC autoantibodies associated with dilatative cardiomyopathy (DCM). The  
 CC invention also describes a chromatographic device comprising (I) bound to  
 CC a solid phase. The products of the invention have cardiotropic activity. (I)  
 CC are useful for treating DCM by binding autoantibodies directed against  
 CC myocardial beta-1-adrenergic receptors, either by neutralizing the  
 CC antibodies in vivo or by extracorporeal treatment of blood or plasma with  
 CC (I) immobilized on a solid phase. This sequence represents a specifically  
 CC claimed peptide used to illustrate the method of the invention.

XX Sequence 14 AA;  
 Query Match 100.0%; Score 55; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.0047;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSFFSELWTS 10  
 Db 2 GSFFSELWTS 11

RESULT 5  
 AAB86013 ID AAB86013 standard; Peptide; 15 AA.  
 XX AC AAB86013;  
 XX DT 12-JUL-2001 (first entry)  
 XX DCM-associated peptide #13.  
 XX DE 19945211-A1.  
 XX KW dilatative cardiomyopathy; autoantibody; cardiotropic;  
 KW beta-1 adrenergic activated antibody; immunosuppressive.  
 XX OS Synthetic.  
 XX PA Key Location/Qualifiers  
 FT Modified-site 15 /note= "N-terminal acetylated"  
 FT Modified-site 15 /note= "C-terminal amide"  
 XX PR 21-SEP-1999; 99DE-01045211.  
 XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;  
 XX DR WPI: 2001-301259/32.  
 XX PD 29-MAR-2001.  
 XX PA 21-SEP-2000; 2000WO-EP0009241.  
 XX PR 21-SEP-1999; 99EP-00118630.  
 XX PR 21-SEP-1999; 99EP-00118631.  
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 PI XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;  
 DR XX WPI: 2001-335469/35.  
 PT New peptide useful for combatting the autoantibodies that are responsible

PT for dilatative cardiomyopathy.  
 XX PS: Claim 4; Page 22; 29pp; German.

XX This invention describes a novel peptide (P1) which can be used for (1)  
 CC isolating beta-1-adrenergic activated antibodies bound to (P1) on a solid  
 CC phase; and (2) a chromatographic apparatus with (P1) bound. The products  
 CC of the invention have cardiotropic and immunosuppressive activity. (P1) is  
 CC used to produce medicine to combat beta-1 adrenergic activated  
 CC autoantibodies having a causal pathobiological relationship with dilatative  
 CC cardiomyopathy. This sequence represents a specifically claimed peptide  
 CC used to illustrate the method of the invention.

XX Sequence 15 AA;  
 Query Match 100.0%; Score 55; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.0051;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFSELWTS 10  
 Db 3 GSFFSELWTS 12

RESULT 6  
 AAB86021 ID AAB86021 standard; peptide; 15 AA.  
 XX AC AAB86021;  
 XX DT 12-JUL-2001 (first entry)  
 XX DE DCM autoantibody-associated peptide #2.  
 XX KW DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiotropic;  
 KW autoantibody; myocardial.  
 XX OS Synthetic.  
 XX PR Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetylated"  
 FT Modified-site 15 /note= "C-terminal amide"  
 XX PR 21-SEP-1999; 99DE-01045211.  
 XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;  
 XX DR WPI: 2001-301259/32.  
 XX PD 29-MAR-2001.  
 XX PA New autoantibody-binding peptides with an amino acid sequence  
 PT corresponding a beta-1-adrenergic receptor group useful for treating  
 PT dilatative cardiomyopathy.

XX PS: Claim 2; Page 5; 8pp; German.

XX This invention describes novel peptides (I) with an amino acid sequence  
 CC corresponding a beta-1-adrenergic receptor group recognized by  
 CC autoantibodies associated with dilatative cardiomyopathy (DCM). The  
 CC invention also describes a chromatographic device comprising (I) bound to  
 CC a solid phase. The products of the invention have cardiotropic activity. (I)  
 CC are useful for treating DCM by binding autoantibodies directed against  
 CC myocardial beta-1-adrenergic receptors, either by neutralizing the  
 CC antibodies in vivo or by extracorporeal treatment of blood or plasma with

(1) immobilized on a solid phase. This sequence represents a specifically claimed peptide used to illustrate the method of the invention

CC	XX	XX	Sequence 15 AA;	Score 100.0%; Score 55; DB 4; Length 15;	Best Local Similarity 100.0%; Prod. No. 0.0051;	Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 85.7%; Pred. No. 1.4e+06;	Matches 6; Conservative 0; Mismatches 1;	Indels 0; Gaps 0;
Query Match	XX	XX	XX	XX	XX	XX	Qy	4 FSEEDWTS 10	XX
Best Local Similarity	100.0%;	Prod. No. 0.0051;	XX	XX	XX	XX	Db	1 FSHLWTS 7	XX
Mismatches	10;	Conservative 0;	XX	XX	XX	XX	RESULT 8	AAU91098	XX
Qy	1 GSFFSELWTS 10		XX	XX	XX	XX	ID	AAU91098 standard; protein; 18 AA.	AC
Db	3 GSFFSELWTS 12		XX	XX	XX	XX	DT	05-JUN-2002 (first entry)	XX
RESULT 7	AAU9130	standard; protein; 8 AA.	XX	XX	XX	XX	DE	Human secreted protein sequence #18.	XX
ID	AAU9130	standard; protein; 8 AA.	XX	XX	XX	XX	XX	Human secreted protein; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; infection; cancer; nervous system disorder; ocular disorder; epithelial cell proliferation; wound healing; skin aging; sunburn; transplantation; chemotaxis; tissue regeneration; food additive; preservative; cytostatic; cardiotonic; antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.	XX
AC	AAB09130;	XX	XX	XX	XX	XX	KW	Human secreted protein; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; infection; cancer; nervous system disorder; ocular disorder; epithelial cell proliferation; wound healing; skin aging; sunburn; transplantation; chemotaxis; tissue regeneration; food additive; preservative; cytostatic; cardiotonic; antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.	XX
DT	06-AUG-2003 (revised)	XX	XX	XX	XX	XX	KW	Human secreted protein; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; infection; cancer; nervous system disorder; ocular disorder; epithelial cell proliferation; wound healing; skin aging; sunburn; transplantation; chemotaxis; tissue regeneration; food additive; preservative; cytostatic; cardiotonic; antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.	XX
DT	30-AUG-2000 (first entry)	XX	XX	XX	XX	XX	KW	Human secreted protein; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; infection; cancer; nervous system disorder; ocular disorder; epithelial cell proliferation; wound healing; skin aging; sunburn; transplantation; chemotaxis; tissue regeneration; food additive; preservative; cytostatic; cardiotonic; antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.	XX
DE	Hepatitis GB virus protein sequence SEQ ID NO:252.	XX	XX	XX	XX	XX	KW	Human secreted protein; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; infection; cancer; nervous system disorder; ocular disorder; epithelial cell proliferation; wound healing; skin aging; sunburn; transplantation; chemotaxis; tissue regeneration; food additive; preservative; cytostatic; cardiotonic; antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.	XX
XX	Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection; detection; characterisation; hepatitis.	OS	OS	OS	OS	OS	KW	Human secreted protein; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; infection; cancer; nervous system disorder; ocular disorder; epithelial cell proliferation; wound healing; skin aging; sunburn; transplantation; chemotaxis; tissue regeneration; food additive; preservative; cytostatic; cardiotonic; antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.	XX
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
XX	Hepatitis GB virus.	XX	XX	XX	XX	XX	XX	XX	XX
OS	OS	OS	OS	OS	OS	OS	XX	PN	WO200218412-A1.
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
XX	XX	XX	XX	XX	XX	XX	XX	PD	07-MAR-2002.
XX	XX	XX	XX	XX	XX	XX	XX	PP	17-JAN-2001; 2001WO-US001384.
XX	XX	XX	XX	XX	XX	XX	XX	PR	28-AUG-2000; 2000US-0228086P.
XX	XX	XX	XX	XX	XX	XX	XX	PR	04-JAN-2001; 2001US-0259516P.
XX	XX	XX	XX	XX	XX	XX	XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	XX	XX	XX	XX	XX	XX	XX	PI	Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
XX	XX	XX	XX	XX	XX	XX	XX	PI	Olsen HS, Moore PA, Wei P, Ebner R, Duan RD, Shi Y, Choi GH;
XX	XX	XX	XX	XX	XX	XX	XX	PI	Fischella M, Ni J;
XX	XX	XX	XX	XX	XX	XX	XX	DR	WPI 2002-269525/31.
XX	XX	XX	XX	XX	XX	XX	XX	DR	N-PADB; ABK54136.
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
XX	XX	XX	XX	XX	XX	XX	XX	PT	Seventeen nucleic acid molecules encoding human secreted proteins, useful for the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
XX	XX	XX	XX	XX	XX	XX	XX	PT	Claim 11; Page 461; 505pp; English.
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
XX	XX	XX	XX	XX	XX	XX	XX	CC	The present invention relates to the isolation of novel human secreted proteins, and the polynucleotide sequences encoding them. The secreted proteins are useful to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The secreted proteins are also useful in diagnosing pathological conditions or susceptibility to a pathological condition. Antibodies to the secreted proteins can also be used in alleviating symptoms associated with disorders and in diagnostic immunoassays (ELISA). Disorders which can be diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cancer, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Parkinson's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAU91081-CC
XX	XX	XX	XX	XX	XX	XX	XX	CC	AAU9148 represent human secreted protein sequences
XX	XX	XX	XX	XX	XX	XX	XX	CC	AAU9148

SQ	Sequence 18 AA;	CC	preservative to increase or decrease storage capabilities.
	Query Match 61.8%; Best Local Similarity 85.7%; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	CC	AAU91148 represent human secreted protein sequences
Qy	4 FSELWTS 10 Db	SQ	Sequence 18 AA;
	3 FSEAWNTS 9		
		Query Match 61.8%; Best Local Similarity 85.7%; Matches 6; Conservative 1; Indels 0; Gaps 0;	Score 34; DB 5; Length 18;
		Qy	4 FSELWTS 10
		Db	3 FSEAWNTS 9
RESULT 9	AAU91081	DT	RESULT 10
ID	AAU91081 standard; protein; 18 AA.	ID	ABG65209 standard; protein; 18 AA.
XX		XX	ABG65209
AC	AAU91081;	AC	ABG65209
XX		XX	Human albumin fusion protein #1884.
DT	05-JUN-2002 (first entry)	DT	27-AUG-2002 (first entry)
XX		XX	Human albumin fusion protein #1884.
DB	Human secreted protein sequence #1.	DB	Human albumin fusion protein #1884.
XX	Human secreted protein; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; infection; cancer;	XX	Albumin fusion protein; therapeutic protein X; human albumin; HA;
	KW nervous system disorder; ocular disorder; epithelial cell proliferation;	XX	KW human serum albumin; HSA; cancer; reproductive disorder;
	KW wound healing; kin ging; sunburn; transplantation; chemotaxis;	XX	KW digestive disorder; immune disorder; endocrine disorder;
	KW tissue regeneration; food additive; preservative; cytostatic; cardiotonic;	XX	KW haematopoietic disorder; neural disorder; connective disorder;
	KW antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.	XX	KW cytosolic; antinfertility; antiinflammatory; antiulcer;
XX	OS Homo sapiens.	XX	KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
XX	PN WO200218412-A1.	XX	KW neuroprotective; anticancer; antimicrobial; antiparkinsonian; anticholinergic; osteopathic; antiarthritic.
PD	07-MAR-2002.	XX	XK Homo Sapiens.
XX	PP 17-JAN-2001; 2001WO-US001384.	XX	OS Synthetic.
XX	PR 28-AUG-2000; 2000US-0228086P.	XX	PR WO200177137-A1.
PR	04-JAN-2001; 2001US-0259516P.	XX	PR 18-OCT-2001.
XX	PA (HUMA-) HUMAN GENOME SCI INC.	XX	PP 12-APR-2001; 2001WO-US011988.
XX	PI Rosen CA, Komatsuouis GA, Baker KP, Birse CE, Soppet DR; Shi Y, Choi GH;	XX	PR 12-APR-2000; 2000US-0223358P.
PI	Olsen HS, Moore PA, Wei P, Ebner R, Duan RD,	PR 25-APR-2000; 2000US-0193384P.	
PI	Fiscella M, Ni J;	PR 21-DEC-2000; 2000US-0255931P.	
XX	DR WPI: 2002-269525/31.	XX	PA (HUMA-) HUMAN GENOME SCI INC.
DR	N-PSDB; ABG54119.	XX	PI Rosen CA, Haseltine WA;
XX	PT Seventeen nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.	XX	DR WPI: 2002-010886/01.
XX	PT in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.	XX	XX New fusion protein for treating disease e.g. diabetes comprises an PT albumin fused to a therapeutic protein.
XX	XX	XX	XX
PS	Claim 11; Page 450; 505pp; English.	PS	The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders, (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia, and connective disorders (e.g. osteoporosis, arthritis).
XX		XX	CC ABG63326 ABG65518 represent albumin fusion proteins of the invention
		XX	CC Sequence 18 AA;
		SQ	CC
CC	The present invention relates to the isolation of novel human secreted proteins, and the polynucleotide sequences encoding them. The secreted proteins are useful to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The secreted proteins are also useful in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the secreted proteins can also be used in alleviating symptoms associated with disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which can be diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cancer, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Parkinson's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or	CC	

Qy	4 FSELWTS 10 Db	 3 FSEAWTS 9	Score 34; DB 5; Length 18; Best Local Similarity 61.8%; Pred. No. 34; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Db	3 FSEAWTS 9
<b>RESULT 11</b>					
ABG65210	ID ABG65210 standard; protein; 18 AA.	XX	AAB86007 standard; peptide; 13 AA.	RESULT 12	
XX	ABG65210;	AC	AAB86007;	XX	
XX	DT -AUG-2002 (first entry)	XX	XX	DT 12-JUL-2001 (first entry)	
XX	Human albumin fusion protein #1885.	DE	DB DCM-associated peptide #7.	XX	
XX	Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiflammatory; antilulcer; immunomodulator; anti-HIV; antidiabetic; haemototic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.	OS	KW DCM; dilatative cardiomyopathy; autoantibody; cardiant; beta-1 adrenergic activated antibody; immunosuppressive.	XX	
XX	Homo sapiens.	OS	Synthetic.	XX	
XX	Synthetic.	OS	WO200121660-A1.	XX	
XX	WO200171137-A1.	PN	PN 2001-335469/35.	XX	
XX	PD 18-OCT-2001.	PD	New peptide useful for combating the autoantibodies that are responsible for dilatative cardiomyopathy.	XX	
XX	PF 12-APR-2001; 2001WO-US011988.	PT	New peptide useful for combating the autoantibodies that are responsible for dilatative cardiomyopathy.	XX	
XX	PR 12-APR-2000; 2000US-0229358P.	PS	Claim 3; Page 21; 29pp; German.	XX	
PR 25-APR-2000; 2000US-0199384P.	CC	This invention describes a novel peptide (P1) which can be used for (1) isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid phase; and (2) a chromatographic apparatus with (P1) bound. The products of the invention have cardiant and immunosuppressive activity. (P1) is used to produce medicine to combat beta-1 adrenergic activated autoantibodies having a causal pathological relationship with dilatative cardiomyopathy. This sequence represents a specifically claimed peptide used to illustrate the method of the invention	XX		
PR 21-DEC-2000; 2000US-0256931P.	CC	XX	XX	XX	
PA (HUMA-) HUMAN GENOME SCI INC.	CC	XX	XX	XX	
XX	Rosen CA, Haseltine WA;	PI	XX	XX	
XX	WI; 2002-010886/01.	DR	XX	XX	
XX	New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein.	PT	Sequence 13 AA;	SQ	
XX	Claim 1; Page 1828; 2102PP; English.	PS	Query Match Score 60.0%; Best Local Similarity 50.0%; Pred. No. 37; Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	Query Match Score 33; Best Local Similarity 50.0%; Pred. No. 37; Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	
XX	The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA), also known as human serum albumin, (HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro, in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).	CC	1 GSFFSELWTS 10 3 GRFLSDWTS 12	1 GSFFSELWTS 10 3 GRFLSDWTS 12	
XX	ABG63326-ABG55518 represent albumin fusion proteins of the invention.	CC	RESULT 13 AAB86014 standard; peptide; 15 AA.	RESULT 13 AAB86014 standard; peptide; 15 AA.	
XX	Sequence 18 AA;	CC	ID AAB86014 standard; peptide; 15 AA. XX	ID AAB86014 standard; peptide; 15 AA. XX	
XX	Query Match Score 34; DB 5; Length 18;	DE	DB DCM-associated peptide #14.	DE	
Best Local Similarity 61.8%; Pred. No. 34;	XX	KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;	XX		
Matches 6; Conservative 6; Mismatches 0; Indels 1; Gaps 0;	OS	KW beta-1 adrenergic activated antibody; immunosuppressive.	XX		
Qy 4 FSELWTS 10	OS	Synthetic.	OS		



CC region of the human plectin 10 protein of the invention

XX Sequence 15 AA;

SQ Query Match 60.0%; Score 33; DB 5; Length 15;  
Best Local Similarity 55.6%; Pred. No. 42;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFFFEELWTS 10

:|||:|:|

Db 2 AFFSSIWLS 10

Search completed: August 27, 2004, 09:25:43

Job time : 127 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 09:22:53 ; Search time 31 Seconds  
(without alignments)

16.654 Million cell updates/sec

Title: AUDET681-1

Perfect score: 55

Sequence: 1 gsfsselwts 10

Scoring table: BLOSUM62

Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 186303

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgnd\_6/prodata/2/iaa/5A\_COMB\_pep:  
2: /cgnd\_6/prodata/2/iaa/5B\_COMB\_pep:  
3: /cgnd\_6/prodata/2/iaa/6A\_COMB\_pep:  
4: /cgnd\_6/prodata/2/iaa/6B\_COMB\_pep:  
5: /cgnd\_6/prodata/2/iaa/PC7US\_COMB\_pep:  
6: /cgnd\_6/prodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	34	61.8	8	4	US 08-469-260A-252	Sequence 252, App
2	34	61.8	8	4	US 08-488-446-252	Sequence 252, App
3	34	61.8	8	4	US 08-467-344A-252	Sequence 252, App
4	31	56.4	18	2	US 08-934-955-125	Sequence 125, App
5	30	54.5	6	1	US 08-124-957-6	Sequence 6, Appli
6	30	54.5	6	3	US 09-035-666-6	Sequence 6, Appli
7	30	54.5	11	1	US 08-424-957-42	Sequence 6, Appli
8	30	54.5	11	3	US 09-035-666-42	Sequence 42, Appli
9	30	54.5	19	4	US 09-081-955-13	Sequence 13, Appli
10	28	50.9	11	3	US 09-186-598-6	Sequence 6, Appli
11	28	50.9	11	3	US 09-669-21A-6	Sequence 6, Appli
12	28	50.9	11	4	US 09-081-276-6	Sequence 6, Appli
13	28	50.9	13	2	US 08-537-39B-388	Sequence 388, App
14	28	50.9	13	3	US 08-871-35A-388	Sequence 388, App
15	28	50.9	13	4	US 09-201-355-388	Sequence 2, Appli
16	27	49.1	6	1	US 08-277-660A-27	Sequence 2, Appli
17	27	49.1	6	1	US 08-124-957-2	Sequence 2, Appli
18	27	49.1	6	3	US 09-035-666-2	Sequence 2, Appli
19	27	49.1	6	4	US 09-081-975-1	Sequence 1, Appli
20	27	49.1	6	4	US 09-128-022B-130	Sequence 130, App
21	27	49.1	7	1	US 08-277-660A-27	Sequence 27, Appli
22	27	49.1	7	1	US 08-424-957-15	Sequence 15, Appli
23	27	49.1	7	1	US 08-124-957-19	Sequence 19, Appli
24	27	49.1	7	3	US 09-035-666-15	Sequence 15, Appli
25	27	49.1	7	3	US 09-035-666-19	Sequence 7, Appli
26	27	49.1	10	1	US 08-277-660A-7	Sequence 11, Appli
27	49.1	10	1	US 08-424-957-11	Sequence 11, Appli	

## ALIGNMENTS

RESULT 1  
US-08-469-260A-252  
; Sequence 252, Application US/08469260A

; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMMY J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SUBRESH M. DESJAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKE  
; APPLICANT: SHEIKI L. BUIK  
; APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3100  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469, 260A  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/424, 550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-938-2623  
TELEFAX: 708-938-2623  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-469-260A-252  
 Query Match 61.8%; Score 34; DB 4; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10  
 Db 1 FSHLWTS 7

RESULT 2  
 US-08-488-446-252 Application US/08488446  
 / Sequence 252, Application US/08488446  
 / Patent No. 6558898  
 / GENERAL INFORMATION:  
 / APPLICANT: JOHN N. SIMONS  
 / APPLICANT: TAMI J. PILOT-MATIAS  
 / APPLICANT: GEORGE J. DAWSON  
 / APPLICANT: GEORGE G. SCHLAUDER  
 / APPLICANT: SURESH M. DESAI  
 / APPLICANT: THOMAS P. LEARY  
 / APPLICANT: ANTHONY SCOTT MUERHOFF  
 / APPLICANT: JAMES C. ERKER  
 / APPLICANT: SHERI L. BUIJK  
 / APPLICANT: ISA K. MUSHAHWAR  
 / TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
 / TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
 / NUMBER OF SEQUENCES: 716  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
 / STREET: 100 ABBOTT PARK ROAD  
 / CITY: ABBOTT PARK  
 / STATE: IL  
 / ZIP: 60064-3500  
 / COMPUTER READABLE FORM:  
 / COMPUTER: IBM PC compatible  
 / MEDIUM TYPE: Floppy disk  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/467,344A  
 / FILING DATE: 07-Jun-1995  
 / CLASSIFICATION: <Unknown>  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 08/424,550  
 / FILING DATE: <Unknown>  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: POREMBSKI, PRISCILLA E.  
 / REGISTRATION NUMBER: 33,207  
 / REFERENCE/DOCKET NUMBER: 5527.PC.01  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 708-937-6365  
 / TELEX/FAX: 708-938-2623  
 / INFORMATION FOR SEQ ID NO: 252:  
 / LENGTH: 8 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: Linear  
 / MOLECULE TYPE: protein  
 / SEQUENCE DESCRIPTION: SEQ ID NO: 252:  
 / US-08-467-344A-252  
 / CLASSIFICATION:  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/424,550  
 / FILING DATE:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: POREMBSKI, PRISCILLA E.  
 / REGISTRATION NUMBER: 33,207  
 / REFERENCE/DOCKET NUMBER: 5527.PC.01  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 708-937-6365  
 / TELEX/FAX: 708-938-2623  
 / INFORMATION FOR SEQ ID NO: 252:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 8 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / US-08-488-446-252  
 / Query Match 61.8%; Score 34; DB 4; Length 8;  
 / Best Local Similarity 85.7%; Pred. No. 3e+05;  
 / Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10  
 Db 1 FSHLWTS 7

RESULT 3  
 US-08-488-446-252  
 / Sequence 252, Application US/08488446  
 / Patent No. 6558898  
 / GENERAL INFORMATION:  
 / APPLICANT: DILLNER, JOAKIM  
 / APPLICANT: DILLNER, LENA  
 / APPLICANT: CHENG, HWE-MING  
 / TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
 / PAPILLOMAVIRUS 1, 5, 6, 8,  
 / TITLLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
 / TITLLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
 NUMBER OF SEQUENCES: 193  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MASON & ASSOCIATES, P.A.  
 STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
 CITY: CLEARWATER  
 STATE: FLORIDA  
 COUNTRY: U.S.A.  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 3.0  
 SOFTWARE: Microsoft Word 6.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/934,915  
 FILING DATE: 22-SEP-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/949, 836  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LOUISE A. Foutch  
 REGISTRATION NUMBER: 37,133  
 REFERENCE/DOCKET NUMBER: 1946.6  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 813-538-3800  
 TELEFAX: 813-538-3820  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 125:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08 934-915-125

Query Match 56.4%; Score 31; DB 2; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 36;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFPSELMT 9  
 Db 5 SFFSRFTWS 12

RESULT 5  
 US-08-424 957-6  
 Sequence 6, Application US/08424957  
 Patent No. 5790377  
 GENERAL INFORMATION:  
 APPLICANT: Lane, David P.  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: Picksley, Steven M.  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fiehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,957  
 FILING DATE: 19-APR-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/424,957  
 FILING DATE: 19-APR-1995  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown

US-09-035-686-6  
 Sequence 6, Application US/09035686  
 Patent No. 6153391  
 GENERAL INFORMATION:  
 APPLICANT: Lane, David P.  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: Lane, David P.  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fiehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/035,686  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/424,957  
 FILING DATE: 19-APR-1995  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown

US-09-035-686-6

Query Match Similarity 54.5%; Score 30; DB 3; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELW 8  
 Db 2 FSELW 6

RESULT 7  
 US-08-424-957-42  
 Sequence 42, Application US/08424957  
 Patent No. 5770317  
 GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flair, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/035,686  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/424,957  
 FILING DATE: 19-APR-1995  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-5249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,957  
 FILING DATE: 19-APR-1995  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-5249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 STRANDEDNESS:  
 TOPOLOGY: unknown

RESULT 8  
 US-08-424-957-42  
 Sequence 42, Application US/09035686  
 Patent No. 6153391  
 GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50

Query Match Similarity 54.5%; Score 30; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 33; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELW 8  
 Db 5 FSELW 9

RESULT 9  
 US-09-081-975-13  
 Sequence 13, Application US/09081975  
 Patent No. 6451919  
 GENERAL INFORMATION:  
 APPLICANT: Keelin, William  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: Jost, Christine  
 TITLE OF INVENTION: METHODS OF TREATMENT USING  
 NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon Peabody LLP  
 STREET: 101 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatibile  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSeq for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/081,975  
 FILING DATE: 12-MAY-1998  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/046,207  
 FILING DATE: 12 MAY 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Eisenstein, Ronald I  
 REGISTRATION NUMBER: 30,628  
 REFERENCE/DOCKET NUMBER: 47400  
 TELECOMMUNICATION: 617-345-6054  
 TELEFAX: 617-345-1300  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQ ID NO: 13

Query Match LENGTH: 11  
 Best Local Similarity 54.5%; Score 30; DB 4; Length 19;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FSSELW 8  
 Db 8 FSSELW 12

RESULT 10 US-09-186-958-6  
 Sequence 6, Application US/09186958B  
 GENERAL INFORMATION:  
 APPLICANT: Whelihan, E. Fayette  
 PATENT NO. 6238860  
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19  
 FILE REFERENCE: DYax-009 0 US sequence listing  
 CURRENT APPLICATION NUMBER: US/09186,958B  
 CURRENT FILING DATE: 1998-11-05  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 6

LENGTH: 11  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19  
 OTHER INFORMATION: binding polypeptide

US-09-186-958-6

Query Match LENGTH: 11  
 Best Local Similarity 50.9%; Score 28; DB 3; Length 11;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 FFSELTWS 10  
 Db 1 FFCAIWPS 8

RESULT 11 US-09-669-271A-6  
 Sequence 6, Application US/09669271A  
 GENERAL INFORMATION:  
 APPLICANT: Whelihan, E. Fayette  
 PATENT NO. 6211197  
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19  
 FILE REFERENCE: Dyax-009 0 US sequence listing  
 CURRENT APPLICATION NUMBER: US/09669,271A  
 CURRENT FILING DATE: 2000-09-26  
 PRIOR APPLICATION NUMBER: 09/186,958  
 PRIOR FILING DATE: 1998-11-05  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 6

LENGTH: 11  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19  
 OTHER INFORMATION: binding polypeptide

US-09-669-271A-6

Query Match LENGTH: 11  
 Best Local Similarity 50.9%; Score 28; DB 3; Length 11;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 FFSELTWS 10  
 Db 1 FFCAIWPS 8

RESULT 12 US-09-881-276-6  
 Sequence 6, Application US/09881276B  
 GENERAL INFORMATION:  
 APPLICANT: Whelihan, E. Fayette  
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19  
 FILE REFERENCE: DYX-009 0 US-2  
 CURRENT FILING DATE: 2001-06-14  
 PRIOR APPLICATION NUMBER: 09/669,271  
 PRIOR FILING DATE: 2000-09-26  
 PRIOR APPLICATION NUMBER: 09/186,958  
 PRIOR FILING DATE: 1998-11-05  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: Microsoft Word 97  
 SEQ ID NO 6

LENGTH: 11  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide

US-09-881-276-6

Query Match LENGTH: 11  
 Best Local Similarity 50.9%; Score 28; DB 4; Length 11;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 FFSELTWS 10  
 Db 1 FFCAIWPS 8

RESULT 13 US-08-637-759B-398  
 Sequence 388, Application US/08637759B  
 GENERAL INFORMATION:  
 APPLICANT: David William Holden  
 TITLE OF INVENTION: Identification of Genes  
 NUMBER OF SEQUENCES: 501  
 CORRESPONDENCE ADDRESS:  
 PATENT NO. 5876931  
 GENERAL INFORMATION:  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30309-3450  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/637,759B

FILING DATE: 03-MAY-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB95/02875  
 FILING DATE: 11-DEC-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31.284  
 REFERENCE/DOCKET NUMBER: RPMS 101  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404) 873-8794  
 TELEFAX: (404) 873-795  
 INFORMATION FOR SEQ ID NO: 388:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 US-08-637-759B-388

Query Match 50.9%; Score 28; DB 2; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 88;  
 Matches 4; Conservative 2; Missmatches 2;  
 Indels 0; Gaps 0;

Qy 3 FFSELWTS 10  
 Db 3 FYSDTMLS 10

---

RESULT 15  
 US-09-201-945-388  
 Sequence 388, Application US/09201945  
 Patent No. 6342215  
 GENERAL INFORMATION:  
 APPLICANT: David William Holden  
 TITLE OF INVENTION: Identification of Genes  
 NUMBER OF SEQUENCES: 501  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 2800 One Atlantic Center  
 STREET: 1201 West Peachtree Street  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30309-3450  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/201,945  
 FILING DATE:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/637,759  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/201,945  
 FILING DATE:  
 CLASIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31.284  
 REFERENCE/DOCKET NUMBER: RPMS 101  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404) 873-8794  
 TELEFAX: (404) 873-8795  
 INFORMATION FOR SEQ ID NO: 388:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 US-09-201-945-388

Query Match 50.9%; Score 28; DB 4; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 88;  
 Matches 4; Conservative 2; Missmatches 2;  
 Indels 0; Gaps 0;

Qy 3 FFSELWTS 10  
 Db 3 FYSDTMLS 10

---

Search completed: August 27, 2004, 09:28:43  
 Job time : 32 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 09:26:14 ; Search time 684 Seconds  
(without alignments)

4.600 Million cell updates/sec

Title: AUDET681-1

Perfect score: 55

Sequence: 1 gsfselfwts 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen Parameters: 268144

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA:  
 1: /cgnd\_6/\_prodatal/2/\_pubpaas/us07\_pubccomb.pep:  
 2: /cgnd\_6/\_prodatal/2/\_pubpaas/pct\_new\_pub.pep:  
 3: /cgnd\_6/\_prodatal/2/\_pubpaas/us06\_pub.pep:  
 4: /cgnd\_6/\_prodatal/2/\_pubpaas/us06\_pubccomb.pep:  
 5: /cgnd\_6/\_prodatal/2/\_pubpaas/us07\_new\_pub.pep:  
 6: /cgnd\_6/\_prodatal/2/\_pubpaas/pctus\_pubccomb.pep:  
 7: /cgnd\_6/\_prodatal/2/\_pubpaas/us08\_new\_pub.pep:  
 8: /cgnd\_6/\_prodatal/2/\_pubpaas/us08\_pubccomb.pep:  
 9: /cgnd\_6/\_prodatal/2/\_pubpaas/us09\_pubccomb.pep:  
 10: /cgnd\_6/\_prodatal/2/\_pubpaas/us09\_pubcomb.pep:  
 11: /cgnd\_6/\_prodatal/2/\_pubpaas/us09\_pubcomb.pep:  
 12: /cgnd\_6/\_prodatal/2/\_pubpaas/us09\_new\_pub.pep:  
 13: /cgnd\_6/\_prodatal/2/\_pubpaas/us10a\_pubcomb.pep:  
 14: /cgnd\_6/\_prodatal/2/\_pubpaas/us10a\_pubcomb.pep:  
 15: /cgnd\_6/\_prodatal/2/\_pubpaas/us10b\_pubcomb.pep:  
 16: /cgnd\_6/\_prodatal/2/\_pubpaas/us10\_new\_pub.pep:  
 17: /cgnd\_6/\_prodatal/2/\_pubpaas/us60\_new\_pub.pep:  
 18: /cgnd\_6/\_prodatal/2/\_pubpaas/us60\_pubcomb.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

## RESULT 1

US-08-424-550B-252 i Sequence 252, Application US/08424550B

i Publication No. US2002119447A1

i GENERAL INFORMATION:

i APPLICANT: JOHN N. SIMONS

i APPLICANT: TAMIL J. PILOT-MATIAS

i APPLICANT: GEORGE J. DAWSON

i APPLICANT: GEORGE G. SCHLAUDER

i APPLICANT: SUBRESH M. DESAI

i APPLICANT: THOMAS P. LEARY

i APPLICANT: ANTHONY SCOTT MUERHOFF

i APPLICANT: JAMES C. ERICKER

i APPLICANT: SHERI L. TUTUIJK

i APPLICANT: ISA K. MUSHAHWAR

i TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

i TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

i NUMBER OF SEQUENCES: 716

i CORRESPONDENCE ADDRESS:

i ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

i STREET: 100 ABBOTT PARK ROAD

i CITY: ABBOTT PARK

i STATE: IL

i COUNTRY: USA

i ZIP: 60064-3500

i COMPUTER READABLE FORM:

i MEDIUM TYPE: Floppy disk

i COMPUTER: IBM PC compatible

i OPERATING SYSTEM: PC-DOS/MS-DOS

i SOFTWARE: Patient Release #1.0, Version #1.25

i CURRENT APPLICATION DATA:

i APPLICATION NUMBER: US/08/424,550B

i FILING DATE:

i CLASSIFICATION: 435435

i ATTORNEY/AGENT INFORMATION:

i NAME: PORENBSK, PRISCILLA E.

i REGISTRATION NUMBER: 133,207

i REFERENCE/DOCKET NUMBER: 5527.PC.01

## SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	34	61.8	8	US-08-424-550B-252 Sequence 252, App
2	34	61.8	18	11 US-09-833-245-1958 Sequence 1958, App
3	34	61.8	18	11 US-09-833-245-1959 Sequence 1959, App
4	30	54.5	10	9 US-09-214-371-35 Sequence 35, App
5	30	54.5	10	9 US-09-214-371-36 Sequence 36, App
6	30	54.5	13	16 US-10-221-042-1 Sequence 1, Appl
7	30	54.5	19	13 US-10-155-059-13 Sequence 53, Appl
8	30	54.5	21	12 US-10-651-563-53 Sequence 35636, A
9	30	54.5	22	9 US-09-864-761-35536 Sequence 36, App
10	29	52.7	15	14 US-10-192-381-46 Sequence 17, App
11	29	52.7	16	14 US-10-224-356-36 Sequence 519, App
12	29	52.7	18	14 US-10-224-356-36 Sequence 519, App
13	29	52.7	21	12 US-10-372-676-519 Sequence 35, App
14	29	52.7	21	14 US-10-097-065-519 Sequence 35, App
15	28	50.9	9	US-09-486-734A-35 Sequence 35, App

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 708-937-6365  
 INFORMATION FOR SEQ ID NO: 252:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US 08-424-550B-252

Query Match 61.8%; Score 34; DB 8; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10  
 Db 1 FSHLWTS 7

---

RESULT 2  
 US 09-B3-245-1958  
 Sequence 1958, Application US/09833245  
 Publication No. US20040010134A1

GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.  
 TITLE OF INVENTION: Albumin Fusion Proteins  
 FILE REFERENCE: PF546PCT

CURRENT APPLICATION NUMBER: US/09/833,245  
 CURRENT FILING DATE: 2001-04-12  
 PRIOR APPLICATION NUMBER: 60/129, 358  
 PRIOR FILING DATE: 2000-04-12  
 PRIOR APPLICATION NUMBER: 60/199, 384  
 PRIOR FILING DATE: 2000-04-25  
 NUMBER OF SEQ ID NOS: 2267  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1958  
 LENGTH: 18  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US -09-833-245-1958

Query Match 61.8%; Score 34; DB 11; Length 18;  
 Best Local Similarity 85.7%; Pred. No. 42;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10  
 Db 3 FSEAWTS 9

---

RESULT 3  
 US -09-833-245-1959  
 Sequence 1959, Application US/09833245  
 Publication No. US20040010134A1

GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.  
 TITLE OF INVENTION: Albumin Fusion Proteins  
 FILE REFERENCE: PF546PCT

CURRENT APPLICATION NUMBER: US/09/833,245  
 CURRENT FILING DATE: 2001-04-12  
 PRIOR APPLICATION NUMBER: 60/229, 358  
 PRIOR FILING DATE: 2000-04-12  
 PRIOR APPLICATION NUMBER: 60/256, 931  
 PRIOR FILING DATE: 2000-04-12  
 PRIOR APPLICATION NUMBER: 60/199, 384  
 PRIOR FILING DATE: 2000-04-25  
 NUMBER OF SEQ ID NOS: 2267  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1959  
 LENGTH: 18  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US -09-833-245-1959

Query Match 61.8%; Score 34; DB 11; Length 18;  
 Best Local Similarity 85.7%; Pred. No. 42;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10  
 Db 3 FSEAWTS 9

---

RESULT 4  
 US -09-214-371-35  
 Sequence 35, Application US/09214371B  
 Patent No. US20010018511A1

GENERAL INFORMATION:  
 APPLICANT: Lane, David  
 APPLICANT: Bottger, Volker  
 APPLICANT: Garcia-Echeverria, Carlos  
 APPLICANT: Furet, Pascal  
 APPLICANT: Pickley, Stephen  
 APPLICANT: Chene, Patrick  
 APPLICANT: Hochkeppel, Heinz-Kurt  
 APPLICANT: Garcia-Echeverria, Carlos  
 APPLICANT: Furet, Pascal  
 TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
 FILE REFERENCE: 4-20937A/PCT  
 CURRENT APPLICATION NUMBER: US/09/214,371B  
 CURRENT FILING DATE: 1999-03-26  
 PRIOR APPLICATION NUMBER: PCT/EP97/03549  
 PRIOR FILING DATE: 1997-07-04  
 NUMBER OF SEQ ID NOS: 83  
 SEQ ID NO: 35  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: peptide  
 NAME/KEY: VARIANT  
 LOCATION: (1)  
 OTHER INFORMATION: X = Ac-Cys (Acrd)  
 NAME/KEY: VARIANT  
 LOCATION: (10)  
 OTHER INFORMATION: X = Pro-NH2  
 US -09-214-371-35

Query Match 54.5%; Score 30; DB 9; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSFFSELW 8  
 Db 2 GPTFSDLW 9

---

RESULT 5  
 US -09-214-371-36  
 Sequence 36, Application US/09214371B  
 Patent No. US20010018511A1

GENERAL INFORMATION:  
 APPLICANT: Lane, David  
 APPLICANT: Bottger, Volker  
 APPLICANT: Pickley, Stephen  
 APPLICANT: Chene, Patrick  
 APPLICANT: Hochkeppel, Heinz-Kurt  
 APPLICANT: Garcia-Echeverria, Carlos  
 APPLICANT: Furet, Pascal  
 TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
 FILE REFERENCE: 4-20937A/PCT  
 CURRENT APPLICATION NUMBER: US/09/214,371B

CURRENT FILING DATE: 1999-03-26  
 PRIORITY NUMBER: PCT/EP97/03549  
 PRIOR FILING DATE: 1997-07-04  
 NUMBER OF SEQ ID NOS: 83  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 36  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:peptide  
 NAME/KEY: VARIANT  
 LOCATION: (1)  
 OTHER INFORMATION: X = Ac-Cys  
 NAME/KEY: VARIANT  
 LOCATION: (1)  
 OTHER INFORMATION: x = PRO-NH2  
 US-09-214-371-36

Query Match Score 54.5%; Score 30; DB 9; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1 GSFFSELW 8
Db	2 GFTFSDLW 9

RESULT 6  
 US-10-221-042-1  
 Sequence 1, Application US/10221042  
 Publication No. US20040120946A1  
 GENERAL INFORMATION:  
 APPLICANT: KANEKA CORPORATION  
 TITLE OF INVENTION: ADSORBENTS FOR DILATED CARDIOMYOPATHY  
 FILE REFERENCE: 12218/5  
 CURRENT APPLICATION NUMBER: US/10/221.042  
 CURRENT FILING DATE: 2002-10-09  
 PRIOR APPLICATION NUMBER: PCT/JP01/03026  
 PRIOR FILING DATE: 2001-04-09  
 PRIOR APPLICATION NUMBER: JP 2000-106915  
 PRIOR FILING DATE: 2000-04-07  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 13  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: peptide

NAME/KEY: MISC FEATURE  
 OTHER INFORMATION: Peptide having a binding affinity for an antibody against M2 muscarinic receptor  
 OTHER INFORMATION: beta-adrenoceptor and/or an antibody against M2 muscarinic receptor

US-10-221-042-1

Query Match Score 54.5%; Score 30; DB 16; Length 13;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 GSFFSEL 7
Db	7 GSFFCEL 13

RESULT 7  
 US-10-155-059-13  
 Sequence 13, Application US/10155059  
 Publication No. US2002147173A1  
 GENERAL INFORMATION:  
 APPLICANT: Kaelin, William Jost, Christine

TITLE OF INVENTION: METHODS OF TREATMENT USING NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE ANTIBODIES  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: Nixon Peabody LLP  
 STREET: 101 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FASTSEQ For Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/155,059  
 FILING DATE: 24-May-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/081,975  
 FILING DATE: 12-MAY-1998  
 APPLICATION NUMBER: 60/046,207  
 FILING DATE: 12-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Eisenstein, Ronald I  
 REGISTRATION NUMBER: 30,628  
 TELEPHONE: 617-345-6054  
 TELEFAX: 617-345-1300  
 TELECOMMUNICATION INFORMATION:  
 REFERENCE/DOCKET NUMBER: 47400  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-10-155-059-13

Query Match Score 54.5%; Score 30; DB 13; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	4 FSELW 8
Db	5       8 FSELW 12

RESULT 8  
 US-10-651-563-53  
 Sequence 53, Application US/10651563  
 Publication No. US20040072952A1  
 GENERAL INFORMATION:  
 APPLICANT: Sachiko MACHIDA  
 APPLICANT: Ken TOKUTASU  
 APPLICANT: Shigeru MATSUMAGA  
 APPLICANT: Yoshiakiyo SAKAKIBARA  
 APPLICANT: Masuko KOBORI  
 APPLICANT: Zheseng WEN  
 TITLE OF INVENTION: Novel Peptide Capable of Specifically Acting on Biological Membran  
 FILE REFERENCE: NF002  
 CURRENT APPLICATION NUMBER: US/10/651,563  
 CURRENT FILING DATE: 2003-08-29  
 PRIOR APPLICATION NUMBER: 2002-253169  
 PRIOR FILING DATE: 2002-08-30  
 PRIOR APPLICATION NUMBER: 2003-21198  
 PRIOR FILING DATE: 2003-01-29  
 NUMBER OF SEQ ID NOS: 122  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 53

LENGTH: 21  
 TYPE: PCT  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: synthetic peptide coded by random DNA library  
 US-10-651-561-53

Query Match 54.5%; Score 30; DB 12; Length 21;  
 Best Local Similarity 62.5%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSFFSELM 8  
 Db 3 GSFPPLLW 10

RESULT 9  
 US-09-864-761-35636  
 ; Sequence 35636, Application US/09864761  
 ; Patent No. US20020043763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rankel, David R.  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: Aeonica-X-1  
 CURRENT APPLICATION NUMBER: US/09/864,761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00660  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: US 09/608,408  
 NUMBER OF SEQ ID NOS: 49117

OTHER INFORMATION: MAP TO AC009946.1  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.8  
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7  
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96  
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9  
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3  
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1  
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8  
 OTHER INFORMATION: EST\_HUMAN HIT: AW452898.1, EVALUATE 5.00e-03  
 US-09-864-761-35636

Query Match 54.5%; Score 30; DB 9; Length 22;  
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFSELM 8  
 Db 5 YFSQW 10

RESULT 10  
 US-10-192-381-46  
 ; Sequence 46, Application US/10192381  
 ; Publication No. US20030170807A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
 ; APPLICANT: WORLEY, Paul  
 ; APPLICANT: TU, Jian  
 ; APPLICANT: XIAO, Bo  
 ; APPLICANT: LEAFY, Daniel  
 ; APPLICANT: BENKEN, Jutta  
 ; APPLICANT: LANAHAN, Anthony  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS FILE REFERENCE: THU1.5.B0-4  
 CURRENT APPLICATION NUMBER: US/10/192,381  
 ; CURRENT FILING DATE: 2003-07-09  
 ; PRIOR APPLICATION NUMBER: US/09/377,285  
 ; PRIOR FILING DATE: 1999-01-18  
 ; PRIOR APPLICATION NUMBER: US 60/138,426  
 ; PRIOR FILING DATE: 1999-06-10  
 ; PRIOR APPLICATION NUMBER: US 60/138,493  
 ; PRIOR FILING DATE: 1999-06-10  
 ; PRIOR APPLICATION NUMBER: US 60/138,494  
 ; PRIOR FILING DATE: 1999-06-10  
 ; PRIOR APPLICATION NUMBER: US 60/097,334  
 ; PRIOR FILING DATE: 1998-08-18  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 46  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-192-381-46

Query Match 52.7%; Score 29; DB 14; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 BLWTS 10  
 Db 8 BLWTS 12

RESULT 11  
 US-10-224-356-36  
 ; Sequence 36, Application US/10224356  
 ; Publication No. US20030144196A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company

SOFTWARE: Amimax Sequence Listing Engine vers. 1.1  
 SEQ ID NO: 35636  
 LENGTH: 22  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:

Page 5

```

// TITLE OF INVENTION: ACTIVATED T LYMPHOCYTE NUCLEIC ACID SEQUENCES AND POLYPEPTIDES EN
// TITLE OF INVENTION: SAME
// FILE REFERENCE: D0033.NP
// CURRENT APPLICATION NUMBER: US/10/224,356
// CURRENT FILING DATE: 2002-08-21
// PRIOR APPLICATION NUMBER: US 60/313,957
// PRIOR FILING DATE: 2001-08-21
// NUMBER OF SEQ ID NOS: 38
// SOFTWARE: PatentIn version 3.1
// SEQ ID NO: 36
// LENGTH: 16
// TYPE: PRT
// ORGANISM: Homo sapiens
// US-10-224-356-36

Query Match      52.7%;  Score 29;  DB 14;  Length 16;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy          1 GSFFSEIW 8
           : ||| |
Db          6 GTRFSEAW 13

RESULT 12
US-10-224-356-17
// Sequence 17, Application US/10224356
// Publication No. US2003014419641
// GENERAL INFORMATION:
// APPLICANT: Bristol-Myers Squibb Company
// TITLE OF INVENTION: ACTIVATED T LYMPHOCYTE NUCLEIC ACID SEQUENCES AND POLYPEPTIDES EN
// TITLE OF INVENTION: SAME
// FILE REFERENCE: D0033.NP
// CURRENT APPLICATION NUMBER: US/10/224,356
// CURRENT FILING DATE: 2002-08-21
// PRIOR APPLICATION NUMBER: US 60/313,957
// PRIOR FILING DATE: 2001-08-21
// NUMBER OF SEQ ID NOS: 38
// SOFTWARE: PatentIn version 3.1
// SEQ ID NO: 17
// LENGTH: 18
// TYPE: PRT
// ORGANISM: Homo sapiens
// US-10-224-356-17

Query Match      52.7%;  Score 29;  DB 14;  Length 18;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy          1 GSFFSEIW 8
           : ||| |
Db          4 GTRFSEAW 11

RESULT 13
US-10-372-876-519
// Sequence 519, Application US/10372876
// Publication No. US20030204071A1
// GENERAL INFORMATION:
// APPLICANT: Moore, Paul A. et al.
// TITLE OF INVENTION: Human Secreted Proteins
// FILE REFERENCE: P2021P1
// CURRENT APPLICATION NUMBER: US/10/372,876
// CURRENT FILING DATE: 2003-02-26
// PRIOR APPLICATION NUMBER: 09/334,595
// PRIOR FILING DATE: 1999-06-17
// PRIOR APPLICATION NUMBER: PCT/US98/27059
// PRIOR FILING DATE: 1998-12-17
// PRIOR APPLICATION NUMBER: 60/070,923
// PRIOR FILING DATE: 1997-12-18
// PRIOR APPLICATION NUMBER: 60/068,007
// PRIOR FILING DATE: 1997-12-18
// PRIOR APPLICATION NUMBER: 60/068,057

```

```

US-10-097-065-519
Query Match      52.7%; Score 29; DB 14; Length 21;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy   1 GSFFSELWT 9
     ||| :|:|
Db   13 GSVYSTIMS 21

RESULT 15
US-09-486-734A-35
Sequence 35, Application US/09486734A
Patent No. US2002016732A1
GENERAL INFORMATION:
APPLICANT: Chopin, Marie-Christine
APPLICANT: Clier, Florence
APPLICANT: Erlich, S. Dusko
APPLICANT: Gautier, Michel
APPLICANT: Schouler, Catherine
APPLICANT: Institut National de la Recherche Agronomique
TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
FILE REFERENCE: 33329/196048
CURRENT APPLICATION NUMBER: US/09/486,734A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/FR98/01873
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: FR 97/10885
PRIOR FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 9
TYPE: PRO
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HsdS subunit
US-09-486-734A-35

Query Match      50.9%; Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy   1 GSFFSEL 7
     ||| :|
Db   2 GSFFKQL 8

```

Search completed: August 27, 2004, 09:48:10  
Job time : 685 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on:

August 27, 2004, 09:19:58 ; Search time 37 Seconds  
(without alignments)

25.998 Million cell updates/sec

Title: AUDET681-1

Perfect score: 55

Sequence: 1 gsfse1wts 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 4494

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

## Listing First 45 summaries

Database :

PIR 78-\*

1: Pir1;\*

2: pir2;\*

3: pir3;\*

4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Match	Length	DB	Description
1	30	54.5	10	C39191	hypothetical protein C39191
2	28	50.9	15	PH1613	Ig H chain V-D-J r
3	25	45.5	12	PT0274	Ig heavy chain CRD
4	24	43.6	7	PH1602	Ig H chain V-D-J r
5	24	43.6	19	S60110	hypothetical protein S60110
6	23	41.8	14	A60622	somatostatin - sp
7	23	41.8	20	A60728	cytochrome P450 3A
8	22	40.0	15	F29501	fibrinopeptide A -
9	22	40.0	16	PH1638	Ig H chain V-D-J r
10	22	40.0	16	SS5125	cysteine-rich secretory protein 1
11	21	38.2	13	PH0138	T-cell receptor beta
12	21	38.2	13	PH1905	collecting duct wall
13	21	38.2	14	A35105	hypothetical protein A35105
14	21	38.2	16	C37290	homeotic protein G
15	21	38.2	17	PH1331	Ig heavy chain DJ
16	21	38.2	19	PH1352	Ig heavy chain DJ
17	21	38.2	19	PH1315	Ig heavy chain DJ
18	21	38.2	19	S57515	T-cell receptor beta
19	21	38.2	20	PA0022	protein QA10001 -
20	21	38.2	20	PH1358	Ig heavy chain DJ
21	20	36.4	6	B34835	dnaA protein - pse
22	20	36.4	10	T13838	cytochrome-c oxidase
23	20	36.4	11	S05002	corazonin - Americ
24	20	36.4	13	S32473	lymnaDPanide 3 - g
25	20	36.4	13	H56046	urinary tract ston
26	20	36.4	13	PH1620	Ig H chain V-D-J r
27	20	36.4	14	C60414	somatostatin - s11
28	20	36.4	14	B60842	somatostatin I - C
29	20	36.4	14	A60840	somatostatin I - E

Query	3 FFSELWTS 10	2 YFSRPTTS 9
Qy	:	
Db	2	YFSRPTTS 9
RESULT 1		
C39191		
hypothetical protein 1 (Tetx' 5' region) - Bacteroides fragilis		
C;Species: Bacteroides fragilis		
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993		
C;Accession: C39191		
R;Speer, B.S.; Bedzyk, L.; Salyers, A.A.		
J;Bacteriol. 173, 176-183, 1991		
A;Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides trar		
A;Reference number: A39191; MUID:91100280; PMID:1846135		
A;Accession: C39191		
A;Status: Preliminary; not compared with conceptual translation		
A;Molecule type: DNA		
A;Residues: 1-10 <SPB>		
A;Cross-references: GB:M37699		
Query Match	54.5%	Score 30; DB 2; Length 10;
Best Local Similarity	62.5%	Pred. No. 17; Mismatches 1; Indels 0; Gaps 0;
Matches	5	Conservative

Query	3 FFSELWTS 10	2 YFSRPTTS 9
Qy	:	
Db	2	YFSRPTTS 9
RESULT 2		
PH1613		
Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)		
C;Species: Mus musculus (house mouse)		
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999		
C;Accession: PH1613		
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.		
J;Exp. Med. 178, 317-329, 1993		
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice		
A;Reference number: PH1580; MUID:93301609; PMID:8315387		
A;Accession: PH1613		
A;Molecule type: DNA		
A;Residues: 1-15 <LEV>		
A;Experimental source: bone marrow pre-B lymphocyte		
C;Keywords: immunoglobulin		
Query Match	50.9%	Score 28; DB 2; Length 15;
Best Local Similarity	57.1%	Pred. No. 60; Mismatches 1; Indels 0; Gaps 0;
Matches	4	Conservative

QY

3 FFSELWTS 9  
2 YFSRPTTS 9

Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT074  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J;Exp. Med. 173, 395-7, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
 A;Reference number: PT0222; MUID:1893102  
 A;Accession: PT024  
 A;Molecule type: DNA  
 A;Residues: 1-12 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 45.5%; Score 25; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 1; Mismatches 2;  
 Qy 4 FSEBDWTS 10  
 Db 3 YSSSWTS 9

RESULT 4

PH1602  
 Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C;Accession: PH1602  
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A;Reference number: PH1580; MUID:93301609; PMID:8315387  
 A;Accession: PH1602  
 A;Molecule type: DNA  
 A;Residues: 1-7 <LEV>  
 A;Experimental source: bone marrow pre-B lymphocyte  
 C;Keywords: immunoglobulin

Query Match 43.6%; Score 24; DB 2; Length 7;  
 Best Local Similarity 80.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 1;

Qy 5 SELNT 9

Db 3 SSLNT 7

RESULT 5

S60110  
 hypothetical protein - human  
 C;Species: Homo sapiens (man)  
 C;Accession: S60110  
 R;Horne, N.M.H.; Hankin, S.; Wilkinson, M.C.; Nunez, C.; Barracough, R.; McLennan, A.G  
 A;Title: Human diadenosine 5',5'-'P(1),P(1)-tetraphosphate pyrophosphohydrolase is a me  
 A;Reference number: S60110; MUID:96067583; PMID:7487923  
 A;Accession: S60110  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-19 <THO>  
 A;Cross-references: EMBL:U30313; NID:gi1050959; PIDN: AAC50276.1; PID:gi1050960  
 Query Match 43.6%; Score 24; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 4.1e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 1; Mismatches 3;

Qy 3 FFSELNTS 10

Db 5 PYREPRWS 12

RESULT 6  
 A60622  
 somatostatin - spotted ratfish  
 C;Species: Hydrologus colliei (spotted ratfish)  
 C;Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 07-May-1999  
 C;Accession: A60622  
 R;Conlon, J.M.  
 Gen. Comp. Endocrinol. 80, 314-320, 1990  
 A;Title: [Ser(51)-somatosatin-14]: isolation from the pancreas of a holocephalan fish, t:  
 A;Reference number: A60622; MUID:91160949; PMID:1991569  
 A;Accession: A60622  
 A;Molecule type: protein  
 A;Residues: 1-14 <CON>  
 C;Superfamily: somatostatin  
 C;Keywords: hormone; neuropeptide; pancreatic islet  
 F13-14/Disulfide bonds: #status experimental

Query Match 41.8%; Score 23; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 4.5e+02;  
 Matches 5; Conservative 2; Mismatches 2;  
 Indels 0; Gaps 0;  
 Qy 2 SFSELNTS 10  
 Db 5 SFFWKFTFS 13

RESULT 7

A60728  
 cytochrome P450 3A, troleandomycin-induced - sheep (fragment)  
 N;Contains: oxidoreductase (EC 1.1.1.-.)  
 C;Species: Ovis sp. (sheep)  
 C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 05-Mar-1999  
 C;Accession: A60728  
 R;Pineau, T.; Galier, P.; Bonfils, C.; Derancourt, J.; Maurel, P.  
 Biochem. Pharmacol. 36, 901-909, 1990  
 A;Title: Purification of a sheep liver cytochrome P-450 from the P450IIIA gene subfamily.  
 A;Reference number: A60728; MUID:90179800; PMID:2310415  
 A;Accession: A60728  
 A;Molecule type: protein  
 A;Residues: 1-20 <PIN>  
 C;Comment: This cytochrome P450 isozyme is a member of the P450IIIA family but is not fu:  
 C;Genetics:  
 A;Gene: CYP3A  
 C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology  
 C;Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductase

Query Match 41.8%; Score 23; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 6.6e+02;  
 Matches 4; Conservative 0; Mismatches 3;  
 Indels 0; Gaps 0;  
 Qy 2 SFFSSLW 8  
 Db 6 SFSSKETW 12

RESULT 8

F29501  
 fibrinopeptide A - wombat  
 C;Species: Vombatidae gen. sp. (wombat)  
 C;Date: 21-Nov-1987 #sequence\_revision 08-Jun-1990 #text\_change 18-Aug-2000  
 C;Accession: F29501  
 R;Blombaek, B.; Blombaek, M.; Hann, C.  
 unpublished result, cited by Blombaek, B., and Blombaek, M., in Chemotaxonomy and Ser:  
 A;Reference number: A29501  
 A;Accession: F29501  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-15 <PRO>  
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 40.0%; Score 22; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 7.4e+02;  
 Matches 4; Conservative 1; Mismatches 1;  
 Indels 0; Gaps 0;

A;Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context of the MHC class II molecule. A;Reference number: PH0135; PMID:9108843; PMID:1702137

A;Accession: PH0138  
A;Molecule type: mRNA  
A;Residues: 1-13 <MRE>  
C;Keywords: T-cell receptor

**RESULT 9**

Query Match 38.2%; Score 21; DB 2; Length 13;  
Best Local Similarity 37.5%; Pred. No. 9.8e+02;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PFSPESE 6  
Db 5 GSFLAE 10

IG H chain V-D-J region (clone B-less 228) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 17-Mar-1999  
C;Accession: PH1638  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1638  
A;Molecule type: DNA  
A;Residues: 1-16 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Species: immunoglobulin

Query Match 40.0%; Score 22; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 7.9e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SELWTT 9  
Db 12 SMLWT 16

**RESULT 10**

cysteine-rich secretory protein-3 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 17-Mar-1999  
C;Accession: S53125; S56161  
R;Schwidentzyk, U.; Haendler, B.; Schleuning, W.D.  
submitted to the EMBL Data Library, March 1995  
A;Description: Isolation and characterization of the androgen-dependent mouse cysteine-rich protein-3  
A;Reference number: S53125  
A;Accession: S53125  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-18 <SCH>  
A;Cross-references: EMBL:X85321  
R;Schwidentzyk, U.; Haendler, B.; Schleuning, W.D.  
Biochim. J. 309, 831-836, 1995  
A;Title: Isolation and characterization of the androgen-dependent mouse cysteine-rich secretory protein-3  
A;Reference number: S56161; MUID:93366959; PMID:7631693  
A;Accession: S56161  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-18 <SC2>  
A;Cross-references: EMBL:X85321

Query Match 40.0%; Score 22; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPFSE 6  
Db 12 SPYSE 16

**RESULT 11**

T-cell receptor beta chain V-D-J region C8 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-May-1997  
C;Accession: PH0138  
R;Martin, R.; Howell, M.D.; Jaraquemada, D.; Flerlage, M.; Richert, J.; Brostoff, S.; Lo J. Exp. Med. 173, 19-24, 1991

Query Match 38.2%; Score 21; DB 2; Length 14;  
Best Local Similarity 30.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SELWTT 9  
Db 2 SFLWT 6

homeotic protein Gsh-3 - mouse (fragment)  
C;Accession: PH0139  
R;Martin, R.; Howell, M.D.; Jaraquemada, D.; Flerlage, M.; Richert, J.; Brostoff, S.; Lo J. Exp. Med. 173, 19-24, 1991

C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 17-Oct-1997  
 C;Accession: C37290; C38809  
 R;Singh, G.; Kaur, S.; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Potter  
 Proc. Natl. Acad. Sci. U.S.A. 88: 10706-10710, 1991  
 A;Title: Identification of 10 murine homeobox genes.  
 A;Reference number: A37290; PMID:1683707  
 A;Accession: C37290  
 A;Status: preliminary; not compared with conceptual translation.  
 A;Molecule type: DNA  
 A;Residues: 1-16 <SIN>  
 C;Superfamily: unassigned homeobox proteins; homeobox homology  
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F;1-14/Domain: homeobox homology (fragment) <HOX>

---

Query Match Score 21; DB 2; Length 16;  
 Best Local Similarity 42.9%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 SFFSBLW 8  
 Db 10 SKFKRMW 16

RESULT 15  
 PH1331  
 Ig heavy chain DJ region (clone C148-106) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1331  
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shans, S.; Rovera, G.  
 J. Exp. Med. 176: 1577-1581, 1992  
 A;Title: Predominance of fetal type DTH joining in young children with B precursor lymph  
 A;Reference number: PH1302; PMID:93094761; PMID:1460419  
 A;Accession: PH1331  
 A;Molecule type: DNA  
 A;Residues: 1-17 <WAS>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match Score 21; DB 2; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 7 LWTS 10  
 Db 9 VWTs 12

Search completed: August 27, 2004, 09:23:33  
 Job time : 40 secs

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5							
Searched: 141681 seqs, 52070155 residues							
Total number of hits satisfying chosen parameters: 1457							
Minimum DB seq length: 0	Maximum DB seq length: 23	Post-processing: Minimum Match 0%	Maximum Match 100%	Listing First 45 summaries	SUMMARIES		
Database : SwissProt_42:*							
Copyright (c) 1993 - 2004 Compugen Ltd.							
OM protein - protein search, using sw model							
Run on: August 27, 2004, 09:19:59 ; Search time 23 Seconds (without alignments)							
Title: AUDET681-1							
Perfect score: 55							
Sequence: 1 gsfifselwts 10							
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5							
Searched: 141681 seqs, 52070155 residues							
Total number of hits satisfying chosen parameters: 1457							
Minimum DB seq length: 0	Maximum DB seq length: 23	Post-processing: Minimum Match 0%	Maximum Match 100%	Listing First 45 summaries	SUMMARIES		
Database : SwissProt_42:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
Query Match Length DB ID Description							
1 21 38.2 16 1 FIBA_EQVAS	P14449 equus asinus	Score 21; Best Local Similarity 66.7%; Score 21; DB 1; Length 16;					
2 20 36.4 11 1 CORZ_PRAM	P11496 periplaneta	Mismatches 4; Pred. No. 7.7e+02; Mismatches 4; Pred. No. 7.7e+02;					
3 20 36.4 13 1 NP3_LYSTM	P80180 lynnaea stata	Indels 0; Gaps 0; Indels 0; Gaps 0;					
4 20 36.4 14 1 SNSI_MYOSC	P87550 myoxocephalus						
5 20 36.4 14 1 SMS_ALMII	P31885 alligator mississippiensis						
6 20 36.4 21 1 PFL3_ECOLI	P13948 escherichia coli						
7 19 34.5 6 1 FARP_MONEX	P41965 moniezia exiguus						
8 19 34.5 15 1 ALB2_TRAASC	P81189 trachemys scripta						
9 18 32.7 9 1 LITR_PHYRO	P08946 phyllomedusa sauvagii						
10 18 32.7 10 1 ARHX_LOCM1	P81626 locusta migratoria						
11 18 32.7 11 1 LEW_TWETH	P05624 thermus thermophilus						
12 18 32.7 11 1 TKNA_SYNCA	P41333 scyliorhinus stellaris						
13 18 32.7 15 1 FTBA_CERSI	P14463 synurus cerasothermus						
14 18 32.7 16 1 FTBA_FELCIA	P14531 felis silvestris						
15 18 32.7 16 1 FTBA_HYLILLA	P14450 hylobates lar						
16 18 32.7 16 1 FTBA_MACFU	P12803 macaca fasciata						
17 18 32.7 16 1 FTBA_MANLE	P14455 mandrillus leucophaeus						
18 18 32.7 16 1 FTBA_ODOHE	P14459 odcoileus hemionus						
20 18 32.7 16 1 FTBA_TAPTE	P14516 tapirus terrestris						
21 18 32.7 17 1 FTBA_PIG	P14460 sus scrofa						
22 18 32.7 18 1 FTBA_CAMDR	P14444 camelus dromedarius						
23 18 32.7 18 1 FTBA_LAMGL	P14454 lama glama						
24 18 32.7 18 1 TOP1_KLEAE	P46155 klebsiella pneumoniae						
25 18 32.7 19 1 FTBA_BISBO	P14441 bacillus subtilis						
26 18 32.7 19 1 FTBA_SUBBU	P14442 bubulus bubalis						
27 18 32.7 19 1 FTBA_MUNMUP	P14457 muttiacus muntiacus						
28 18 32.7 19 1 FTBA_SHEEP	P14451 ovis aries						
29 18 32.7 23 1 PQQA_SESEAE	P92800 pseudomonas aeruginosa						
30 18 32.7 23 1 PQQA_PSEPK	P98844 pseudomonas fluorescens						
31 18 32.7 23 1 PQQA_PSEPU	P99871 pseudomonas leucophaga						
32 17.5 31.8 8 1 LCK5_BEUMA	P04548 periplaneta americana						
33 17.5 31.8 8 1 HTF1_PERAM	P04548 periplaneta americana						
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5							
Searched: 141681 seqs, 52070155 residues							
Total number of hits satisfying chosen parameters: 1457							
Minimum DB seq length: 0	Maximum DB seq length: 23	Post-processing: Minimum Match 0%	Maximum Match 100%	Listing First 45 summaries	SUMMARIES		
Database : SwissProt_42:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
Query Match Length DB ID Description							
1 21 38.2 16 1 FIBA_EQVAS	P14449 equus asinus	Score 21; Best Local Similarity 66.7%; Score 21; DB 1; Length 16;					
2 20 36.4 11 1 CORZ_PRAM	P11496 periplaneta	Mismatches 4; Pred. No. 7.7e+02; Mismatches 4; Pred. No. 7.7e+02;					
3 20 36.4 13 1 NP3_LYSTM	P80180 lynnaea stata	Indels 0; Gaps 0; Indels 0; Gaps 0;					
4 20 36.4 14 1 SNSI_MYOSC	P87550 myoxocephalus						
5 20 36.4 14 1 SMS_ALMII	P31885 alligator mississippiensis						
6 20 36.4 21 1 PFL3_ECOLI	P13948 escherichia coli						
7 19 34.5 6 1 FARP_MONEX	P41965 moniezia exiguus						
8 19 34.5 15 1 ALB2_TRAASC	P81189 trachemys scripta						
9 18 32.7 9 1 LITR_PHYRO	P08946 phyllomedusa sauvagii						
10 18 32.7 10 1 ARHX_LOCM1	P81624 locusta migratoria						
11 18 32.7 11 1 LEW_TWETH	P05624 thermus thermophilus						
12 18 32.7 11 1 TKNA_SYNCA	P41333 scyliorhinus stellaris						
13 18 32.7 15 1 FTBA_CERSI	P14463 synurus cerasothermus						
14 18 32.7 16 1 FTBA_FELCIA	P14531 felis silvestris						
15 18 32.7 16 1 FTBA_HYLILLA	P14450 hylobates lar						
16 18 32.7 16 1 FTBA_MACFU	P12803 macaca fasciata						
17 18 32.7 16 1 FTBA_MANLE	P14455 mandrillus leucophaeus						
18 18 32.7 16 1 FTBA_ODOHE	P14459 odcoileus hemionus						
20 18 32.7 16 1 FTBA_TAPTE	P14516 tapirus terrestris						
21 18 32.7 17 1 FTBA_PIG	P14460 sus scrofa						
22 18 32.7 18 1 FTBA_CAMDR	P14444 camelus dromedarius						
23 18 32.7 18 1 FTBA_LAMGL	P14454 lama glama						
24 18 32.7 18 1 TOP1_KLEAE	P46155 klebsiella pneumoniae						
25 18 32.7 19 1 FTBA_BISBO	P14441 bacillus subtilis						
26 18 32.7 19 1 FTBA_SUBBU	P14442 bubulus bubalis						
27 18 32.7 19 1 FTBA_MUNMUP	P14457 muttiacus muntiacus						
28 18 32.7 19 1 FTBA_SHEEP	P14451 ovis aries						
29 18 32.7 23 1 PQQA_SESEAE	P92800 pseudomonas aeruginosa						
30 18 32.7 23 1 PQQA_PSEPK	P98844 pseudomonas fluorescens						
31 18 32.7 23 1 PQQA_PSEPU	P99871 pseudomonas leucophaga						
32 17.5 31.8 8 1 LCK5_BEUMA	P04548 periplaneta americana						
33 17.5 31.8 8 1 HTF1_PERAM	P04548 periplaneta americana						
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5							
Searched: 141681 seqs, 52070155 residues							
Total number of hits satisfying chosen parameters: 1457							
Minimum DB seq length: 0	Maximum DB seq length: 23	Post-processing: Minimum Match 0%	Maximum Match 100%	Listing First 45 summaries	SUMMARIES		
Database : SwissProt_42:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
Query Match Length DB ID Description							
1 21 38.2 16 1 FIBA_EQVAS	P14449 equus asinus	Score 21; Best Local Similarity 66.7%; Score 21; DB 1; Length 16;					
2 20 36.4 11 1 CORZ_PRAM	P11496 periplaneta	Mismatches 4; Pred. No. 7.7e+02; Mismatches 4; Pred. No. 7.7e+02;					
3 20 36.4 13 1 NP3_LYSTM	P80180 lynnaea stata	Indels 0; Gaps 0; Indels 0; Gaps 0;					
4 20 36.4 14 1 SNSI_MYOSC	P87550 myoxocephalus						
5 20 36.4 14 1 SMS_ALMII	P31885 alligator mississippiensis						
6 20 36.4 21 1 PFL3_ECOLI	P13948 escherichia coli						
7 19 34.5 6 1 FARP_MONEX	P41965 moniezia exiguus						
8 19 34.5 15 1 ALB2_TRAASC	P81189 trachemys scripta						
9 18 32.7 9 1 LITR_PHYRO	P08946 phyllomedusa sauvagii						
10 18 32.7 10 1 ARHX_LOCM1	P81624 locusta migratoria						
11 18 32.7 11 1 LEW_TWETH	P05624 thermus thermophilus						
12 18 32.7 11 1 TKNA_SYNCA	P41333 scyliorhinus stellaris						
13 18 32.7 15 1 FTBA_CERSI	P14463 synurus cerasothermus						
14 18 32.7 16 1 FTBA_FELCIA	P14531 felis silvestris						
15 18 32.7 16 1 FTBA_HYLILLA	P14450 hylobates lar						
16 18 32.7 16 1 FTBA_MACFU	P12803 macaca fasciata						
17 18 32.7 16 1 FTBA_MANLE	P14455 mandrillus leucophaeus						
18 18 32.7 16 1 FTBA_ODOHE	P14459 odcoileus hemionus						
19 18 32.7 17 1 FTBA_TAPTE	P14516 tapirus terrestris						
20 18 32.7 18 1 FTBA_PIG	P14460 sus scrofa						
21 18 32.7 18 1 FTBA_CAMDR	P14444 camelus dromedarius						
22 18 32.7 18 1 FTBA_LAMGL	P14454 lama glama						
23 18 32.7 18 1 FTBA_BISBO	P46155 klebsiella pneumoniae						
24 18 32.7 18 1 TOP1_KLEAE	P14441 bacillus subtilis						
25 18 32.7 19 1 FTBA_BISBO	P14442 bubulus bubalis						
26 18 32.7 19 1 FTBA_SUBBU	P14457 muttiacus muntiacus						
27 18 32.7 19 1 FTBA_MUNMUP	P14451 ovis aries						
28 18 32.7 19 1 FTBA_SHEEP	P92800 pseudomonas aeruginosa						
29 18 32.7 23 1 PQQA_SESEAE	P98844 pseudomonas fluorescens						
30 18 32.7 23 1 PQQA_PSEPK	P99871 pseudomonas leucophaga						
31 18 32.7 23 1 PQQA_PSEPU	P04548 periplaneta americana						
32 17.5 31.8 8 1 LCK5_BEUMA	P04548 periplaneta americana						
33 17.5 31.8 8 1 HTF1_PERAM	P04548 periplaneta americana						
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5							
Searched: 141681 seqs, 52070155 residues							
Total number of hits satisfying chosen parameters: 1457							
Minimum DB seq length: 0	Maximum DB seq length: 23	Post-processing: Minimum Match 0%	Maximum Match 100%	Listing First 45 summaries	SUMMARIES		
Database : SwissProt_42:*							

RESULT 3  
 TISSUE=Corpora cardiaca;  
 MEDLINE=89325572; PubMed=2753132;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach.";  
 RT PIR: 250:231-234(1989).  
 CC -!- FUNCTION: Cardioactive Peptide. Corazonin is probably involved in the physiological regulation of the heart beat.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 DR PIR: S05002; S05002.  
 KW Neuropептид; Amidation; Pyrrrolidone carboxylic acid.  
 FT MOD RES 1 1 AMIDATION.  
 FT MOD RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1387 MW; C7CEFP32D6415AB46 CRC64;  
 Query Match 36.4%; Score 20; DB 1; Length 11;  
 Best Local Similarity 42.9%; Pred. No. 7.9e+02; Indels 0; Gaps 0;  
 Matches 3; Conservative 2; Mismatches 2;  
 Qy 4 FSELWTS 10 :| |: Db 5 YSREWTN 11

RESULT 4  
 NP\_1YMMT STANDARD; PRT; 13 AA.  
 ID P80180;  
 AC 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Lympna-DF amide 3.  
 OS Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora; Lymnaeoidea; Lymnaeidae; Lymnaea.  
 NCBI\_TAXID=6523;  
 RN [1]  
 RP SEQUENCE.  
 TISSUE=Ganglion;  
 MEDLINE=3238777; PubMed=8477756;  
 RA Johnsen A.H., Rehfeld J.F.;  
 RT "LymnaeDFamides, new family of neuropeptides from the pond snail, *Lymnaea stagnalis*. Clue to cholecystokinin immunoreactivity in invertebrates?";  
 RT Bur. J. Biocem. 213:875-879(1993).  
 CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.  
 DR PIR: S32473; S32473.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 13 13 AMIDATION.  
 FT UNSURE 12 12 AMIDATION.  
 SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5DB865 CRC64;

Query Match 36.4%; Score 20; DB 1; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 1; Mismatches 1;

Qy 1 GSFFPSE 6 :| |: Db 7 GSAFSD 12

RESULT 5  
 SMS\_ALLMI STANDARD; PRT; 14 AA.  
 ID SMS\_ALLMI  
 AC P31885; 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DB SomatoStatin-14.  
 OS Alligator mississippiensis (American alligator), and Trachemys scripta (Red-eared slider turtle) (*Pseudemy's scripta*);  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodyliaidae; Alligatorinae; Alligator.  
 OX NCBI\_TAXID=8496; 34903;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=A.mississippiensis; TISSUE=Stomach;  
 RX MEDLINE=93124451; PubMed=8101369;  
 RA Wang Y., Conlon J.M.;  
 DE SomatoStatin I.  
 OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin), Oncorhynchus kisutch (Coho salmon), and Anguilla anguilla (European freshwater eel).  
 OS Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC .OC

RP	SEQUENCE;	Qy	2 SFFS 5
RC	SPECIES=T. scripta;	DB	
RX	MEDLINE=90341082; PubMed=1974347;		18 SFFS 21
RA	Conlon J.M., Hicks J.W.;		
RT	"Isolation and structural characterization of insulin, glucagon and somatostatin from the turtle, <i>Pseudemys scripta</i> .";		
RT	Peptides 11:461-466 (1990).		
RL	!- SUBCELLULAR LOCATION: Inhibits the release of somatotropin.		
CC	!- FUNCTION: Somatostatin inhibits the release of somatotropin.		
CC	-!- SIMILARITY: Belongs to the somatostatin family.		
DR	PIR; C60414; C60414.		
DR	InterPro; IPR00250; Somatostatin.		
DR	PFAM; PF03002; Somatostatin; 1.		
KW	Hormone.		
FT	DISULFIDE DISULFIDE 3 14 BY SIMILARITY.		
SQ	SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;		
Query Match	Best Local Similarity 36.4%; Score 20; DB 1; Length 14;		
Matches	2 SFFSELENTS 10		
Qy	Best Local Similarity 44.4%; Pred. No. 1e+03;		
Db	4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;		
Query Match	Best Local Similarity 36.4%; Score 20; DB 1; Length 14;		
Matches	2 SFFSELENTS 10		
Qy	Best Local Similarity 44.4%; Pred. No. 1e+03;		
Db	4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;		
RESULT 6	PIL3_ECOLI STANDARD; PRT; 21 AA.		
ID	PIL3_ECOLI		
AC	P13948;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-JAN-1990 (Rel. 13, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Fimbrial protein precursor (Pilin) (Fragment).		
GN	TRAA.		
OS	Escherichia coli.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Escherichia.		
OX	NCBI_TaxID=562;		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=87008371; PubMed=3531163;		
RA	Firlay B.B., Frost L.S.; Parashchyn W.;		
RT	"Origin of transfer of IncF plasmids and nucleotide sequences of the type II oriT, traM, and traY alleles from ColB4-K98 and the type IV traY allele from R100-1."		
RT	J. Bacteriol. 168:132-139 (1986).		
RL	SEXPEIUS ARE FILAMENTOUS SURFACE APPENDAGES REQUIRED FOR CELL-TO-CELL CONTACT DURING BACTERIAL CONJUGATION.		
CC	-!- SUBCELLULAR LOCATION: Secreted.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
CC	EMBL: M15135; AAB04666_1; -.		
DR	InterPro; IPR008873; TraA.		
DR	PFam; PF0513; TraA; 1.		
KW	Plasmid; Conjugation; Fimbria.		
FT	PROBEP 1 >21		
FT	NON_TER 21 21		
SQ	SEQUENCE 21 AA; 2198 MW; 076C0D0C5E9D14EA CRC64;		
Query Match	Best Local Similarity 36.4%; Score 20; DB 1; Length 21;		
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	Best Local Similarity 100.0%; Pred. No. 1.5e+03;		
Db	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
RESULT 7	FARP_MONEX STANDARD; PRT; 6 AA.		
ID	FARP_MONEX		
AC	P41966;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	FMRamide-like neuropeptide GNFRF-amide.		
OS	Moniezia expansa (Sheep tapeworm).		
OC	Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda.		
OC	Cyclopolyllidae; Anopiocephalidae; Moniezia.		
NCBI_TaxID=28841;			
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=93312289; PubMed=83232531;		
RA	Shaw C., Halton D.W., Thim L.;		
RT	"GNFRamide: a novel FMRFamide-immunoreactive peptide isolated from the sheep tapeworm, <i>Moniezia expansa</i> ."		
RL	Biochem. Biophys. Res. Commun. 193:1054-1060 (1993).		
CC	-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.		
CC	DR; PIR: A43129; A43129.		
CC	RW; Neuropeptide; Amidation.		
CC	ET; MOD_RFS 6 AMIDATION.		
SQ	SEQUENCE 6 AA; 787 MW; 69409CS04481000 CRC64;		
Query Match	Score 19; DB 1; Length 6;		
Matches	3; Best Local Similarity 75.0%; Score 19; DB 1; Length 6;		
CC	3; Conservative 1; Mismatches 1; Pred. No. 1.4e+03; Indels 0; Gaps 0;		
Qy	1 GSFF 4		
Db	1 GSFF 4		
RESULT 8	ALB2_TRASC STANDARD; PRT; 15 AA.		
ID	ALB2_TRASC		
AC	P81189;		
DT	15-JUL-1998 (Rel. 36, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	28-SEP-2003 (Rel. 41, Last annotation update)		
DE	68 kDa serum albumin (Alb-2) (Fragment).		
OS	Trachemys scripta (Red-eared slider turtle) ( <i>Pseudemys scripta</i> ).		
OC	Testudines; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.		
NCBI_TaxID=34903;			
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=98103404; PubMed=9440230;		
RA	Brown M.A., Chambers G.K., Licht P.;		
RT	"Purification and partial amino acid sequences of two distinct albums from turtle plasma."		
RT	Comp. Biochem. Physiol. 118B:3367-3374 (1997).		
RL	-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.		
CC	-!- SUBCELLULAR LOCATION: Secreted.		
CC	-!- TISSUE SPECIFICITY: Plasma.		
CC	-!- MISCELLANEOUS: In the red-eared slider turtle, there are two forms of albumin, Alb-1 and Alb-2.		
CC	-!- SIMILARITY: Belongs to the ALB/Arp/VDB family.		
CC	DR; InterPro; IPR00204; Serum albumin.		
DR	PROSITE; PS00212; ALBUMIN; PARTIAL.		
KW	Metal-binding; Lipid-binding.		
FT	NON_TER 15 15		
SQ	SEQUENCE 15 AA; 1733 MW; 4B7422B89FF73223 CRC64;		

Query Match Score 19; DB 1; Length 15;  
Best Local Similarity 34.5%; Pred. No. 1.6e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GSFFSEL 7  
Db 9 GHXFEXL 15

RESULT 9  
LITR PHYRO STANDARD; PRT; 9 AA.

AC P08946;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Rhodei-litorinae.

OS Phyllomedusa rohdei (Rohde's leaf frog).  
Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
OC Phyllomedusinae; Phylomedusa.

OX NCBI\_TAXID=8394; [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;  
RX MEDLINE=85127560; PubMed=3818283;  
RA Barra D., Ersperer G.F., Simmaco M., Bossa F., Melchiorri P.,  
RA Ersperer V.  
RL FEBS Lett. 182:53-56 (1985).

CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin family.

CC PIR; S07241; S07241.  
DR InterPro; IPR000874; Bombesin.  
DR PFAM; PF02044; Bombesin.  
DR PROSITE; PS00357; BOMBESIN; 1.  
DR Amphibian defense peptide; Bombesin; 1.  
KW Pyrrolidone carboxylic acid.

FT MOD RES 1 1 AMIDATION.

SQ SEQUENCE 9 AA; 1090 MW;  
Score 18; DB 1; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ELWTS 10  
:||:  
Db 1 QWAT 5

RESULT 10  
ID AKHX LOCMI STANDARD; PRT; 10 AA.

AC P81676;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Acridoidea; Acridiidae; Oedipodinae; Locusta.  
NCBI\_TAXID=7004; [1]

RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RA Siegert K.J.; Submitted (DEC-1998) to Swiss-Prot.  
-!- FUNCTION: Probably involved in the regulation of locust

CC intermediary metabolism, behavior and/or development.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC Belongs to the AKH / HRTH / EPCH family.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1222 MW;  
Score 18; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FSBLWT 9  
Db 4 FSDWWS 9

RESULT 11  
LPW THETH STANDARD; PRT; 11 AA.

AC P05624;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Trp operon leader peptide.

GN TRPL.  
OS Thermus thermophilus.  
OC Bacterium; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
OC Thermus.

NCBI\_TAXID=274; [1]

RN RP SEQUENCE FROM N.A.  
STRAIN=HB8 / ATCC 27634;  
RX MEDLINE=9900081; PubMed=2844259;  
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;  
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus  
trpE and trpG." RLL Biochim. Biophys. Acta 950:303-312 (1988).  
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS  
OF TRYPTOPHAN.

This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
or send an email to license@isb-sib.ch).

CC DR EMBL\_X07744; CAA30565.; -!  
TRYPTOPHAN biosynthesis; Leader Peptide.

RESULT 12  
TKNA\_SCYCA STANDARD; PRT; 11 AA.

AC P41333;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

OS Scyliorhinus canicula (Spotted catshark).  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acriomorpha;  
OC Acriidoidea; Acridiidae; Oedipodinae; Locusta.

OX DE Substance\_P.  
RN SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RA Siegert K.J.; Submitted (DEC-1998) to Swiss-Prot.  
-!- FUNCTION: Spotted catfish (Spotted catshark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii;  
 OC Scyliorhinidae; Scyliorhinus.  
 OX NCBI\_TAXID=7830;  
 RN [1]  
 RP  
 SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=9329508; PubMed=7685693;  
 RA Waugh D.; Wang Y.; Razon N.; Balment R. J.; Conlon J. M.;  
 RT "Primary structures and biological activities of substance-P-related  
 peptides from the brain of the dogfish, *Scyliorhinus canicula*.";  
 RL Eur. J. Biochem. 214:469-474 (1993).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 evoke behavioral responses, are potent vasoconstrictors and  
 secrete hormones, and contract (directly or indirectly) many smooth  
 muscles.  
 CC -!- SUBCELLULAR LOCATION: Belongs to the tachykinin family.  
 DR PIR: S33300; S33300;  
 DR PROSITE: PS00267; TACHYKININ 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1278 MW; 214860DEBC9D6D867 CRC64;  
 Query Match Score 18; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GSFF 4  
 Db 5 QOFF 8

RESULT 13  
 FIBA\_SYNCA STANDARD; PRT; 15 AA.  
 ID FIBA\_SYNCA  
 AC P14463;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).  
 GN FGA.  
 OS Syncerus caffer (Cape Buffalo).  
 OC Mammalia; Eutheria; Cetartiodactyla; Craniata; Vertebrata; Bovoidea;  
 OC Bovidae; Bovinae; Syncerus.  
 OX NCBI\_TAXID=11;

RP  
 SEQUENCE.  
 RX MEDLINE=6209145; PubMed=6033721;  
 RA Doolittle R.F.; Schubert D.; Schwartz S.A.;  
 RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.  
 Dromedary camel, mule deer, and cape buffalo.";  
 RL Arch. Biochem. Biophys. 118:456-467 (1967).  
 CC -!- FUNCTION: Fibrinogen has double function: yielding monomers that  
 polymerize into fibrin and acting as a cofactor in platelet  
 aggregation.  
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -!- PTM: Conversion of Fibrinogen to fibrin is triggered by thrombin,  
 which cleaves fibrinopeptides A and B from alpha and beta chains,  
 and thus exposes the N-terminal polymerization sites responsible  
 for the formation of the soft clot.  
 KW Blood coagulation; Plasma.  
 FT PEPTIDE 1 15 FIBRINOPEPTIDE A.  
 SQ SEQUENCE 15 AA; 1480 MW; 4E998EA5F0B41CC6 CRC64;

Query Match Score 18; DB 1; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

KW Blood coagulation; plasma.  
PT PEPTIDE 1 16 FIBRINOPEPTIDE A.  
FT NON-TER 16 16 C3C98EB2D6CC7D3 CRC64;  
SQ SEQUENCE 16 AA; 1620 MW;  
Query Match 32.7%; Score 18; DB 1; Length 16;  
Best Local Similarity 50.0%; Pred. No. 2.e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GSFFSE 6  
| | :|  
Db 6 GEFIAE 11

Search completed: August 27, 2004, 09:26:09  
Job time : 26 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 27, 2004, 09:19:59 ; Search time 112 Seconds  
(without alignments)  
28.171 Million cell updates/sec

Title: AUDET681-1

Perfect score: 55  
Sequence: 1 gsfsselwts 10

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Maximum Match 0%

Listing First 45 summaries

Database :

```

1: sp_archea;*
2: sp_bacteria;*
3: sp_fungi;*
4: sp_human;*
5: sp_invertebrate;*
6: sp_mammal;*
7: sp_mythic;*
8: sp_organelle;*
9: sp_phage;*
10: sp_plant;*
11: sp_rabbit;*
12: sp_virus;*
13: sp_vertebrate;*
14: sp_unclassified;*
15: sp_virus;*
16: sp_bacterioplasm;*
17: sp_archaea;*

```

Description :

RESULT 1

Q8HKI2

ID Q8HKI2 PRELIMINARY;

AC Q8HKI2;

DT 01-MAR-2003 [TREMBLrel. 23, Created)

DT 01-MAR-2003 [TREMBLrel. 23, Last sequence update)

DT 01-JUN-2003 [TREMBLrel. 24, Last annotation update)

DE NADH dehydrogenase subunit 1 (Fragment).

GN ND1.

OS Apomomma concolor (echidna tick).

OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Parasitiformes; Ixodida; Ixodidae; Aponomma.

OX NCBI\_TAXID=65640;

RN [1]

RA SEQUENCE FROM N.A.

RA Campbell, N.J.H., Murrell, A., Barker, S.C.;

RT "The value of idiosyncratic markers and conserved tRNA sequences from

RT the mitochondrial genome of hard ticks (Acaria: Ixodidae) for

RT phylogenetic inference."

RL Submitted (Oct 2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY059185; AAU79389.; -.

DR GO:0005739;

KW Mitochondrion.

FT NON\_TER 1 1 MW: E50DD046AD639 CRC64;

SQ SEQUENCE 18 AA: 2241 AA; Score 26; DB 8;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8	22	Q69346 human herpesvirus	
12	22	40.0	12	Q9TRT7 bos taurus	
13	22	40.0	6	Q9tr88 lilium longiflorum	
14	22	40.0	16	Q7Y1X8	
15	22	40.0	17	Q8hKH6 apomomma un	
16	22	40.0	18	Q9s8i7 oryza sativus	

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HKI2 apomomma co	
2	24	43.6	11	Q77895 oreochromis	
3	24	43.6	11	Q77896 oreochromis	
4	24	43.6	22	Q9w6D7 gallus gallus	
5	24	43.6	23	Q9trcs canis familiaris	
6	23	41.8	11	P83537 lactobacillus	
7	23	41.8	13	Q9xi12 benisia tabaci	
8	23	41.8	15	Q9r5ds chromatium	
9	23	41.8	16	Q8qgal brachydanio	
10	23	41.8	20	Q86T45	
11	23	41.8			

AC	077895;	08; Created)	DT	01-NOV-1998 (TREMBLrel.	12; Last sequence update)	DT	01-NOV-1998 (TREMBLrel.	12; Last annotation update)
DT	01-NOV-1998 (TREMBLrel.	08; Last sequence update)	DT	01-JUN-2003 (TREMBLrel.	24; Last annotation update)	DT	01-JUN-2003 (TREMBLrel.	24; Last annotation update)
DT	01-DEC-2001 (TREMBLrel.	19; Last annotation update)	DB	Hydroxyindole-o-methyltransferase isoform A (Fragment).		DB	Hydroxyindole-o-methyltransferase isoform A (Fragment).	
DE	MHC class II B locus 12 (Fragment).		OS	Gallus Gallus (Chicken).		OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	
OS	Oreochromis niloticus (Nile tilapia).		OC			OC		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Teleostei; Buteleosteii; Neoteleosteii; OC		OC			OC		
OC	Acanthomorpha; Acanthopterygii; Perciformes; Labroidei; Cichlidae; Oreocharomis.		NCBI_TaxID=9031;			NCBI_TaxID=8128;		
RN	[1]		RN	[1]		RN	[1]	
RP	SEQUENCE FROM N.A. PubMed=9649539;		RP	SEQUENCE FROM N.A. PubMed=9851690;		RP	SEQUENCE FROM N.A. PubMed=9851690;	
RX	Medline:98315113;		RX	Medline:99057015;		RX	Medline:99057015;	
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincsek V., Figueroa F., Sultmann H., Klein J.;	"Linkage relationships and haplotype polymorphism among cichlid mhc class II B loci"; Genetics 149:1527-1537(1998).	RA	Grechez-Cassiau A.; Bernard M.; Djajali K.; Rodriguez I.R.; Voisin P.; Gene.";	"Structural analysis of the chicken hydroxyindole-O-methyltransferase gene.";	RA	Grechez-Cassiau A.; Bernard M.; Djajali K.; Rodriguez I.R.; Voisin P.; Gene.";	"Structural analysis of the chicken hydroxyindole-O-methyltransferase gene.";
RT			RL	Europ. J. Biochem. 258:44-52(1998).		RT	Europ. J. Biochem. 258:44-52(1998).	
RT			DR	EMBL; AF116455; AAD23444.1;		RT	EMBL; AF116455; AAD23444.1;	
RT			DR	GO; GO:0008168; F:methyltransferase activity; IEA.		RT	GO; GO:0008168; F:methyltransferase activity; IEA.	
RL			DR	GO; GO:0016740; P:transferase activity; IEA.		RL	GO; GO:0016740; P:transferase activity; IEA.	
RL			KW	Methyltransferase; Transferase.		RL	Methyltransferase; Transferase.	
DR			FT	NON_TER 1 1		FT	NON_TER 1 1	
FT			SQ	SEQUENCE 22 AA; 2783 MW; 35726EABF1E450C8 CRC64;		SQ	SEQUENCE 22 AA; 2783 MW; 35726EABF1E450C8 CRC64;	
FT			Query Match	Score 24; DB 7; Length 11;	Score 24; DB 13; Length 22;	Query Match	Score 24; DB 13; Length 22;	Score 24; DB 13; Length 22;
NON_TER	1 1	11	Best Local Similarity	43.6%; Pred. No. 7.e+02;	Best Local Similarity 60.0%; Pred. No. 1.5e+03;	Best Local Similarity 60.0%; Pred. No. 1.5e+03;	Best Local Similarity 60.0%; Pred. No. 1.5e+03;	Best Local Similarity 60.0%; Pred. No. 1.5e+03;
SEQUENCE	11 AA;	1367 MW;	Matches	50.0%; Conservative 2;	Mismatches 2;	Mismatches 2;	Mismatches 2;	Mismatches 2;
FT			Qy	3 FFSELWTS 10	0;	Qy	4 FSELW 8	0;
NON_TER	1 1	11	Matches	4; Conservative 2;	Indels 0;	Db	12 FADLW 16	0;
SEQUENCE	11 AA;	1367 MW;	FT			FT		
FT			RESULT 3			RESULT 5		
NON_TER	1 1	11	Q9TRC6		PRELIMINARY;	Q9TRC6		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9TRC6;	PRT; 23 AA.	ID	Q9TRC6;	PRT; 23 AA.
FT			AC	Q9TRC6;		AC	Q9TRC6;	
NON_TER	1 1	11	Query Match	Score 24; DB 7; Length 11;	Score 24; DB 13; Length 22;	Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Best Local Similarity	43.6%; Pred. No. 7.e+02;	Best Local Similarity 60.0%; Pred. No. 1.5e+03;	Best Local Similarity 57.1%; Pred. No. 1.5e+03;	Best Local Similarity 57.1%; Pred. No. 1.5e+03;	Best Local Similarity 57.1%; Pred. No. 1.5e+03;
FT			Matches	50.0%; Conservative 2;	Mismatches 2;	Mismatches 2;	Mismatches 2;	Mismatches 2;
NON_TER	1 1	11	Qy	3 FFSELWTS 10	0;	Qy	2 SFSEELW 8	0;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			RESULT 6		
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT; 22 AA.	ID	P83537	PRT; 22 AA.
FT			AC	P83537;		AC	P83537;	
NON_TER	1 1	11	Q9W6D7			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
SEQUENCE	11 AA;	1367 MW;	Db	3 FWSMLW 8	0;	Db	6 SFXGETW 12	0;
FT			RESULT 4			Query Match	Score 24; DB 6; Length 23;	Score 24; DB 6; Length 23;
NON_TER	1 1	11	Q9W6D7		PRELIMINARY;	P83537		PRELIMINARY;
SEQUENCE	11 AA;	1367 MW;	ID	Q9W6D7	PRT			

OC	Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC	Chromatiales; Allochromatium.
RN	NCBI_TaxID=1049;
RP	SPOUSE, AND INDUCTION.
RC	SRAINT-DSM 20451;
RX	PubMed=12112860;
RA	Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT	"High pressure effects step-wise altered protein expression in Lactobacillus safranensis.",
RT	Proteomics 2:765-774 (2002).
RL	-!
RT	INDUCTION: BY ELEVATED HYDROSTATIC PRESSURE.
CC	-! MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 65 kDa.
FT	NON_TER 1 1
FT	NON_TER 11 11
FT	SEQUENCE 11 AA; 1249 MW; D966231B771ADD9 CRC64;
QY	1 GSFFFS 5   :   :   : 1 GSFFFA 5
Db	
RESULT 7	
ID	Q9XL12_1 PRELIMINARY;
AC	Q9XL12_1; (TREMBLrel. 12, Created)
DT	01-JUN-1999 (TREMBLrel. 12, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Cytochrome oxidase I (Fragment).
OS	Bemisia tabaci (Sweetpotato whitefly).
OG	Mitochondrion.
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleurodidae; Aleyrodoidea; Aleyrodidae; Aleyrodinae; Bemisia.
OC	Aleyrodoidea; Aleyrodidae; Aleyrodinae; Bemisia.
OX	NCBI_TaxID=7038;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Pubmed=1658381;
RA	Frohlich D.R., Torres-Jerez I., Bedford I.D., Martham P.G., Brown J.K.;
RT	"A phylogeographical analysis of the <i>Bemisia tabaci</i> species complex based on mitochondrial DNA markers.",
RT	Mol. Ecol. B:1683-1691 (1999).
DR	EMBL: AF11003; AA22415.1;
GO	GO:0005739; C:mitochondrion; IEA.
KW	Mitochondrion.
FT	NON_TER 1 1
FT	SEQUENCE 13 AA; 1639 MW; BDD68729F5744365 CRC4;
QY	2 SFFSELW 8   :   :   : 1 SYFTSSW 7
Db	
RESULT 8	
ID	Q9R5D6 PRELIMINARY;
AC	Q9R5D6; (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	POLY (3-HYDROXYBUTYRIC acid) granule-associated 41 kDa protein (Fragment).
DE	Chromatium vinosum.
OS	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC	Chromatiales; Allochromatium.
RN	NCBI_TaxID=1049;
RP	SEQUENCE.
RA	Medline=93146381; PubMed=1490603;
RT	"Isolation and identification of granule-associated proteins relevant for poly(3-hydroxyalkanoic acid) biosynthesis in <i>Chromatium vinosum</i> D.",
RT	FEMS Microbiol. Lett. 78:227-232 (1992).
RL	SEQUENCE 15 AA; 1874 MW; 165FA916BCA2AD CRC64;
QY	2 SFFSELW 8   :   :   : 5 NFENDW 11
Db	
RESULT 9	
ID	Q8QGA1 PRELIMINARY;
AC	Q8QGA1; (TREMBLrel. 21, Created)
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE	Insulin-like growth factor-1b (Fragment).
GN	IGFB1B.
OS	Brachydanio rerio (Zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7935;	
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Gong H.Y., Hu M.C., Chen M.C., Weng C.F., Lin C.J.F., Lin G.H., Wu J.L.;
RA	"The characterization of prepro-insulin-like growth factor-1 Ea-2 expression and insulin-like growth factor-1 genes (devoid 81 bp) in the zebrafish (Danio rerio).", Gene 268:67-75 (2001).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Gong H.Y., Hu M.C., Chen M.H.C., Chen M.C., Weng C.F., Lin C.J.F., Lin G.H., Wu J.L.;
RA	"Developmental expression of zebrafish HNF19, a novel hepatocyte nuclear factor-1 in zebrafish pronephros formation.",
RT	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL	EMBL: AF4B6298; AAL92052.1; -.
DR	NON_TER 16 1913 MW; 1D0A5A4F917EE868 CRC64;
FT	SEQUENCE 16 AA;
QY	1 GSFFSELW 8   :   :   : 4 GHFFQFW 11
Db	
RESULT 10	
ID	Q96T45 PRELIMINARY;
AC	Q96T45; (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-DEC-2003 (TREMBLrel. 24, Last annotation update)
DE	MER receptor tyrosine kinase (Fragment).
OS	Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;

RN [1] SEQUENCE FROM N.A. MEDLINE=20517330; PubMed=11062461;

RX Gal A., Li Y.; Thompson D.A.; Weir J.; Orth U.; Jacobson S.G., Apelstedt-Sylla E.; Vollrath D.;  
 RA "Mutations in MERTK, the human orthologue of the RCS rat retinal dystrophy gene, cause retinitis pigmentosa.", Nat. Genet. 26:270-271 (2000).

RN [2] SEQUENCE FROM N.A. MEDLINE=20017330; PubMed=11062461;

RX Gal A., Li Y.; Thompson D.A.; Weir J.; Orth U.; Jacobson S.G., Apelstedt-Sylla E.; Vollrath D.;  
 RA Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

RX EMBL; AF366303; AAK54121.1;

DR GO:0016301; F:kinase activity; IBA.

DR GO:0004872; F:receptor activity; IBA.

KW Kinase; Receptor.

FT NON\_TER 20 20 AA; 2232 MW; A853BEF/FECE2910 CRC64;

SQ SEQUENCE 20 AA; 2232 MW; A853BEF/FECE2910 CRC64;

Query Match Score 23; DB 4; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GSFFSELW 8  
 Db 11 GLFLPALW 18

RESULT 11  
 ID Q69346 PRELIMINARY; PRT; 22 AA.

AC Q69346; PRELIMINARY; PRT; 22 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DT 34K Protein (Fragment).

DE Human herpesvirus 1.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Simplexvirus.

OX NCBI\_TaxID=10298;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=17; MEDLINE=7010565; PubMed=3020164;

RX Davison B.A.J.; Scott J.E./

RT "DNA Sequence of the Major Capsid Protein Gene of Herpes Simplex virus."; EMBL; X04467; CAA28153.1; -

DR GO:0013067; P: viral assembly, maturation, egress, and rel. . . ; IEA.

DR InterPro; IPR007629; Herpes UL20.

DR Pfam; PF04544; Herpes UL20; 1.

FT NON\_TER 1 1 SEQUENCE 22 AA; 2484 MW; 2CBA43.B3E4C1A0B CRC64;

Query Match Score 23; DB 12; Length 22;  
 Best Local Similarity 42.9%; Pred. No. 2.3e+03; Indels 0; Gaps 0;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFSELWT 9  
 Db 6 FLARFWT 12

RESULT 12  
 Q9TRT7 PRELIMINARY; PRT; 12 AA.

Q9TRT7 PRELIMINARY; PRT; 13, Created)

AC Q9TRT7; PRELIMINARY; PRT; 12 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE Male gametic cell-specific (fragment).

GN LGCl.

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE 15 kDa amyloid protein A homolog (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Bovinae; Bos.

OC NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE; MEDLINE=92132498; PubMed=1734497;

RX Veiby O.P.; Sletten K.; Husby G.; Nordstoga K.; "Amino acid sequence analyses of non-AA proteins from amyloid fibrils of bovine kidney"; Scand. J. Immunol. 35:63-69(1992).

FT NON\_TER 1 1  
 FT NON\_TER 12 12  

SQ SEQUENCE 12 AA; 1503 MW; 64CDB543C6DB4AEB CRC64;

Query Match Score 22; DB 6; Length 12;  
 Best Local Similarity 50.1%; Pred. No. 1.9e+03; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFPSSELW 8  
 Db 1 SFPSXEW 7

RESULT 13  
 Q9TR8B PRELIMINARY; PRT; 16 AA.

ID Q9TR8B  
 AC Q9TR8B; PRELIMINARY; PRT; 16 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-JUN-2003 (TREMBLrel. 14, Last sequence update)

DE PA28 protein (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Bovinae; Bos.

NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE; MEDLINE=95081084; PubMed=7989312;

RX Mott J.D.; Pramanik B.C.; Moonaw C.R.; Afendis S.J.; DeMartino G.N., Slaughter C.A.; "PA28, an activator of the 20 S proteasome, is composed of two nonidentical but homologous subunits.," J. Biol. Chem. 269:31466-31471(1994).

DR GO:0008537; C:proteasome activator complex; IEA.

DR InterPro; IPR00186; PA28\_beta.

DR PF02252; PA28\_beta; 1.

SQ SEQUENCE 16 AA; 1898 MW; 126D340D14EE9BDE CRC64;

Query Match Score 22; DB 6; Length 16;  
 Best Local Similarity 42.9%; Pred. No. 2.5e+03; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SFPSSELW 8  
 Db 1 : : : : 1 AFYAEYL 7

RESULT 14  
 Q7Y1X8 PRELIMINARY; PRT; 17 AA.

ID Q7Y1X8  
 AC Q7Y1X8; PRELIMINARY; PRT; 17 AA.

DT 01-OCT-2003 (TREMBLrel. 25, Created)

DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Male gametic cell-specific (fragment).

GN LGCl.

OS *Lilium longiflorum* (Trumpet lily).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; *Lilium*.  
 OX NCBI\_TAXID=4690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22615576; PubMed=12729996;  
 RA Singh M., Bhalla P.L., Xu H., Singh M.B.;  
 RT "Isolation and characterization of a flowering plant male gametic  
 cell-specific promoter[1].";  
 RT FEBS Lett 542:47-52 (2003).  
 RL EMBL; AY207012; AAP37155.1/-.  
 DR EMBL; AY207012; AAP37155.1/-.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1880 MW; 661B63484969679F CRC64;

Query Match 40.0%; Score 22; DB 10; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 4 FSEBLW 8  
 Db 11 FSSVW 15

---

RESULT 15

Q8HKK6 PRELIMINARY; PRT: 18 AA.  
 ID Q8HKK6  
 AC Q8HKK6;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE NADH dehydrogenase subunit 1 (Fragment).  
 GN NDL.  
 OS *Aponomma undatum* (goanna tick).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; *Aponomma*.  
 OX NCBI\_TAXID=65642;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Campbell N.J.H., Murrell A., Barker S.C.;  
 RT "The value of idiosyncratic markers and conserved tRNA sequences from  
 the mitochondrial genome of hard ticks (*Acari: Ixodida: Ixodidae*) for  
 phylogenetic inference.";  
 RT Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 RL EMBL; AY059193; AAL79395.1/-.  
 DR GO; GO:005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 18 AA; 2362 MW; 1AE724D04CC8D631 CRC64;  
 Query Match 40.0%; Score 22; DB 8; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 2 SFPSSEMT 9  
 Db 10 SFCSINWT 17

Search completed: August 27, 2004, 09:28:10  
 Job time : 118 secs

BLANK